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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/EP99/05652 <b>(22) International Filing Date:</b> 4 August 1999 (04.08.99) <b>(30) Priority Data:</b> 98202634.6 4 August 1998 (04.08.98) EP <b>(71) Applicant (for all designated States except US):</b> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECH- NOLOGIE [BE/BE]; Rijvisschestraat 120, B-9052 Zwij- naarde (BE). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LEE, Jeong, Hee [KR/BE]; Spinnmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). <b>(74) Agent:</b> DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		<b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished          upon receipt of that report.</i>
<b>(54) Title:</b> GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS  <b>(57) Abstract</b> <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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### Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant  
5 molecular biology. In particular, the invention relates to improvements of crop  
productivity of useful plants. One of the major limitations of crop productivity is the  
effect of environmental stress conditions on plant growth and development. An  
important goal of molecular biology is the identification and isolation of genes that can  
provide resistance or tolerance to such stresses. For agriculture, the creation of  
10 transgenic plants containing such genes provides the potential for improving the stress  
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on  
the growth of plants and the productivity of crops. The physiological response to these  
stresses arises out of changes in cellular gene expression. Expression of a number of  
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;  
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be  
classified into two groups: those that directly protect against environmental stresses  
and those that regulate gene expression and signal transduction in the stress  
response. The first group includes proteins that likely function by protecting cells from  
20 dehydration, such as the enzymes required for biosynthesis of various  
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,  
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,  
Bray et al., 1997). The second group of gene products includes transcription factors,  
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et  
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is  
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms  
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the  
30 hypothesis that the genetic information for tolerance to environmental stress conditions  
exists in all higher plants. In glycophytes, this information would only be expressed in  
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:  
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of  
35 evidence also demonstrate that even mild environmental stress conditions throughout  
the growth season have a negative impact on plant growth and crop productivity. It is

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for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by a non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO<sub>2</sub> etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

5 "Dehydration stress" is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole plant.

"Drought stress" refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

"Oxidative stress" refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms "salinity-induced stress", "salt-stress" or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

15 The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

20 The terms "tolerance" and "resistance" cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability, productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

30 The terms "tolerance" and "resistance" may be used interchangeably in the present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 $\mu$  plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5 The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996),  
10 Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is  
15 chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30 Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH. The T<sub>m</sub> is the temperature (under defined ionic strength and pH) at which  
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent  
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1  
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or  
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having  
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid  
30 comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,  
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DFB2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (e) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (c) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 10 (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 35 (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;



- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74, more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not  
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the  
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence  
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means  
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of  
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and  
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5       The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10       The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression in these systems.

15       The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress of said plant.

20       The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

25       The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

30       Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonosoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably  
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method  
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a  
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a  
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a  
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,  
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said  
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid or indirectly increases or induces the protein activity of a protein encoded by said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence" meaning that said recombinant DNA molecule will comprise a sequence originating from a foreign species, or, if from the same species, may be substantially modified from its original form. For example, a promoter operably linked to a structural gene which is from a species different from which the structural gene was derived, or, if from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein of the invention as defined above. According to this embodiment, other polynucleic acids modulating the expression or the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.



For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of  
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,  
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of  
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and  
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example  
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The  
35 introduced sequence generally will be substantially identical to the endogenous

sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with  
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of  
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose  
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the  
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control  
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard  
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in  
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,  
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter  
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,  
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the  
35 following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative  
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a  
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can  
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,  
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

25 Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress  
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of  
35 the present invention can be employed to produce transgenic stress tolerant plant with



any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- 15 (xi) alteration of alkaloid and/or cardiac glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype 25 to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or 30 tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5 The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10 The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein  
15 having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

The present invention also relates to the cloning of the genomic counterpart of  
20 any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present  
25 invention also relates to the coding region as well as the promoter region of any of said genomic clones.

The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30 The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the  
35 primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references  
5 mentioned herein are incorporated by reference.

## BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast *Dbf2* (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2* sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3 ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37° C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut für Züchtungsforschung, Köln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing *At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H<sub>2</sub>O<sub>2</sub> (oxidative stress) and incubated at 28°C or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut für Züchtungsforschung, Köln, Germany).

5           Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to  
10   OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

          Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during  
15   plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown  
20   in b and d using a PhosphorImager (Molecular Dynamics).

          Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
25   section) upon applying a salt stress of 200 mM NaCl overnight.

          Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
30   section) upon applying an osmotic stress induced by 20% PEG overnight.

          Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until -7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H<sub>2</sub>O<sub>2</sub>, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H<sub>2</sub>O<sub>2</sub> (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

20

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

+	:	similar growth to the DY wild type cells;
++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
++++	:	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

35



Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

## **EXAMPLES**

### **Example 1. Construction of the cDNA library.**

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H<sub>2</sub>O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)<sub>14</sub>-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

### **Example 2. Yeast transformation and selection for osmotolerance.**

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietel, 1995). After transformation with the Arabidopsis cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected Arabidopsis cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected Arabidopsis cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD<sub>600</sub> at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

### Example 3. Characterization of *At-DBF2*.

*At-DBF2*, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward *et al.* 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks *et al.* (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

### Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae* *DBF2* enhances cold, heat, salt and drought tolerance in yeast.

In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

**Example 5. Both *At-DBF2* and *DBF2* can functionally complement the *hog1* mutation.**

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-BDF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the overexpression of both *DBF2* and *At-DBF2* (Figure 4).

**Example 6. *At-DBF2* is cell cycle regulated.**

*DBF2* expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul *et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*, 1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

**Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction**

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

**Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells**

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

#### **Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress**

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

#### **Example 10. Tolerance to environmental stress in plant cells**

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-*CaMVter*. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control transgenic calli.

**Example 11. Tolerance to environmental stress in plants.**

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefore seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,



70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l<sup>-1</sup> sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

#### Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N ; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 gm<sup>-3</sup> denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA.

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR ; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

**Tabel 1**

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dictyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent - kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 - sequence	107	+++	++++
unknown	chromosome 4 - sequence	109	+	++++
unknown	chromosome 5 - sequence	111	++++	+++
unknown	chromosome 5 - sequence	113	++++	++
unknown	chromosome 5 - sequence	115	++++	++++
unknown	chromosome 5 - sequence	117	+	++++
unknown	chromosome 5 - sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
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**TABLE 2**  
**EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF**  
**THE PRESENT INVENTION**

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
$\alpha$ -amylase ( <i>Amy32b</i> )	Aleurone	Lanahan <i>et al</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin $\beta$ -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
chalcone synthase ( <i>chsA</i> )	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; <a href="http://winetitles.com.au/gwrdc/csh95-1.html">http://winetitles.com.au/gwrdc/csh95-1.html</a>
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AtPRP4	Leaf	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
$\beta$ -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
RD2 gene	root cortex	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
TobRB7 gene	root vasculature	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
AtPRP4	leaves; flowers; lateral root primordia	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczyński <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
LEAFY	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
CLAVATA1	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
Blz2	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate synthase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993



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### Claims

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
  - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
  - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
  - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
  - (a) SEQ ID NO 1, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

(a) SEQ ID NO 3, or the complementary strand thereof;

(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

15

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

20

9. Use of an isolated polynucleic acid as defined above which is chosen from:

(a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

25

(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

30

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

35

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:

- (a) SEQ ID NO 5, or the complementary strand thereof;
- 5 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- 10 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined  
15 in any of claims 2 to 10, or a functional fragment thereof.

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of  
SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40,  
42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,  
20 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or  
120.

13. A method for producing a plant with enhanced tolerance or resistance to  
environmental stress, said method comprising transiently introducing into a plant  
25 cell a recombinant DNA comprising a polynucleic acid of or as defined in any of  
claims 2 to 10 which is expressed in an amount effective to confer enhanced  
tolerance or resistance to environmental stress.

14. A method for producing a plant with enhanced tolerance or resistance to  
30 environmental stress, said method comprising stably introducing into a plant cell a  
recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2  
to 10 which is expressed in an amount effective to confer enhanced tolerance or  
resistance to environmental stress.



15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.
- 5 16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.
- 10 17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.
- 15 18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
  - a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 20
19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,
- 25
- 30

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

- 5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.
- 10 21. A recombinant polynucleic acid comprising:  
a polynucleic acid according to or as defined in any of claims 2 to 10, and,  
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 15 22. A recombinant polynucleic acid comprising:  
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,  
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant  
25 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.
24. The recombinant polynucleic acid of claim 21 comprising at least part of the  
30 nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
- 5 26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
- 10 28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
- 15 30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
- 20 32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
- 25 34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
- 35 35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.
- 35

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

At-DBF2	.....MAGNMSCLS TOGHGTPGSGGHFPNQNLTKRRTRPAGINDSPSPVKCFFFPYEDTSNTSLKEYSQPTKYSNSPPVSPAI FVERATSWCT	89
DBF2	MLSKSEKNVDLLAGNMSNLSFDGHGTPGGTGLFPNQNLTKRRTRPAGINDSPSPVKPSFFPYEDTSNMDIDEVSPQDMDVSNSPKKLPKFFYERATSNKT	100
At-DBF2	QRVWSGRAMYFLEYCDMFDYVVISRRQRTKQVLEYLQQQSQLPNSDQIKLNEEWSSYLQREHQVLSKRRLKPKNHRDFEMITQVGGGYGHVYLARKKOTK	189
DBF2	QRVWSVKHMYFLEHYCDMFDYVVISRRQRTKQVLEYLQQQSQLPNSDQIKLNEEWSSYLQREHQVLSKRRLKPKNHRDFEMITQVGGGYGVVYLARKKOTK	200
At-DBF2	EVCALKILNKKLGFKLNGTCHVLTERRQSLTTTRSETMVKLLSGTTPVSGRGNATSESELGGDFRTESIGRRCLKSGHARFYISEMFCVAVNEKHLLSKT...	287
DBF2	EVCALKILNKKLLFKLNETKHVLTERRDILTTTRSENLVKLLYAFQDLQSLYLAMEFVPGGDFRTLLINTRCLKSGHARFYISEMFCVAVNALHDLGYTHRD	300
At-DBF2	.....DSTISNEEDSSINIRLEKEKDLGYPALSEKSIEDRKLY.....TCPNSMVGSPDYIALEVLGRKRYEYTVQYWS	356
DBF2	LKPENFLIDAKGHIKLTDFGLAAGTISNERIESMKIRLEKIKOLEPFAFTSEKSIDRRKMYNOLREKINYANSMVGSPDYMALEVLGKGYDFTVQYWS	400
At-DBF2	LGCMLFESLVGYTPFGSGSTNETYATISRSWKQTLNRAHEDGRAAFYNRTWDLITRHRADLSTRTSRFEHVKHNSYFADILFKALRSIPPFPPQLDSET	456
DBF2	LGCMLFESLVGYTPFGSGSTNETYDNLRRUKQTLRRPRQSDGRAAFSDRTWDLITRLTADPINLRLSFEHVKHNSYFADINFSTLRSWIPPFPPQLDSET	500
At-DBF2	DAGYFDDFWNEADIAKYADVFNQQCORTALVDDSAVSSKLVGFTFRHRNGKGGSSGMLFNGLEHSDPFSTFY	528
DBF2	DAGYFDDFTSEADMAKYADVFKRQDKLTANVDDSAVSSKLVGFTFRHRNGKGGSSGMLFNGLEHSDPFSTFY	572

FIGURE 1 A

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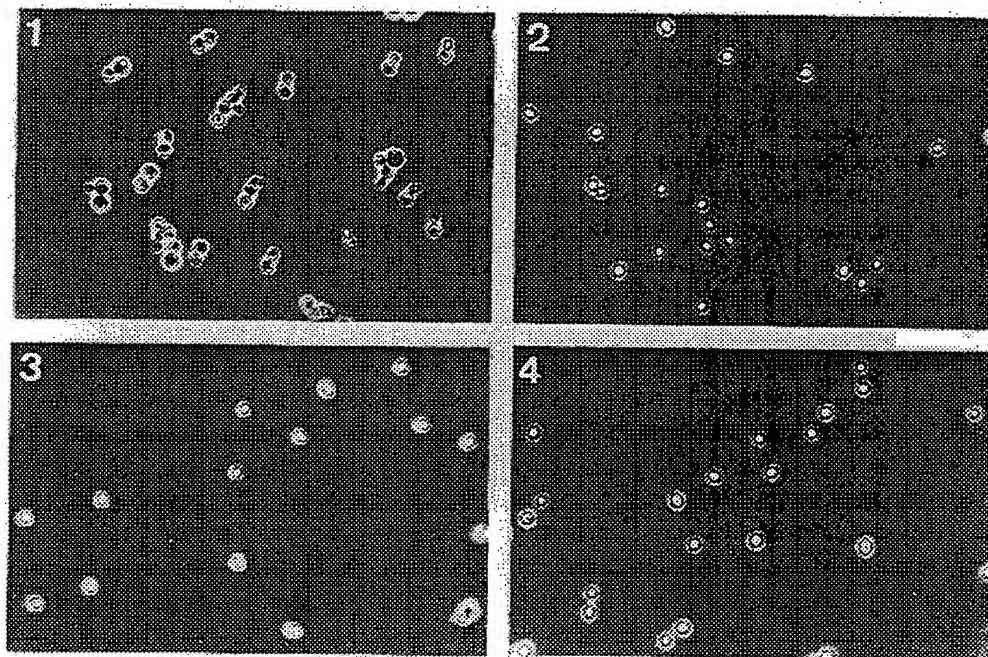


FIGURE 1B

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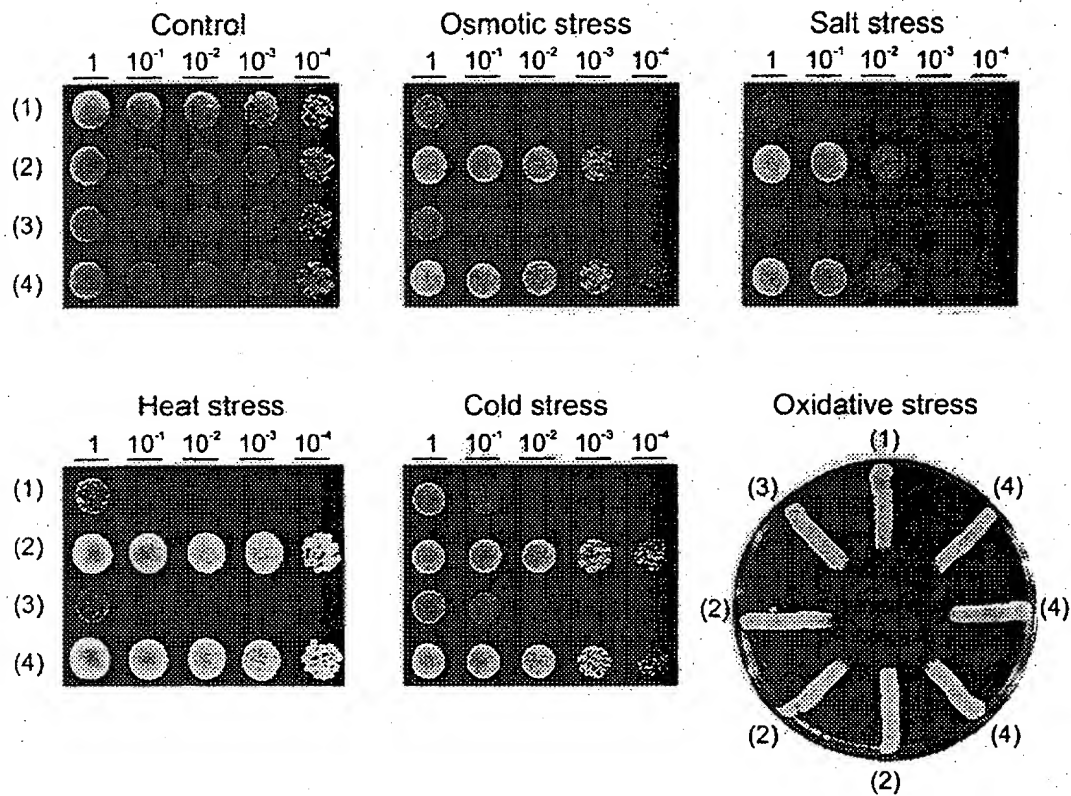


FIGURE 2

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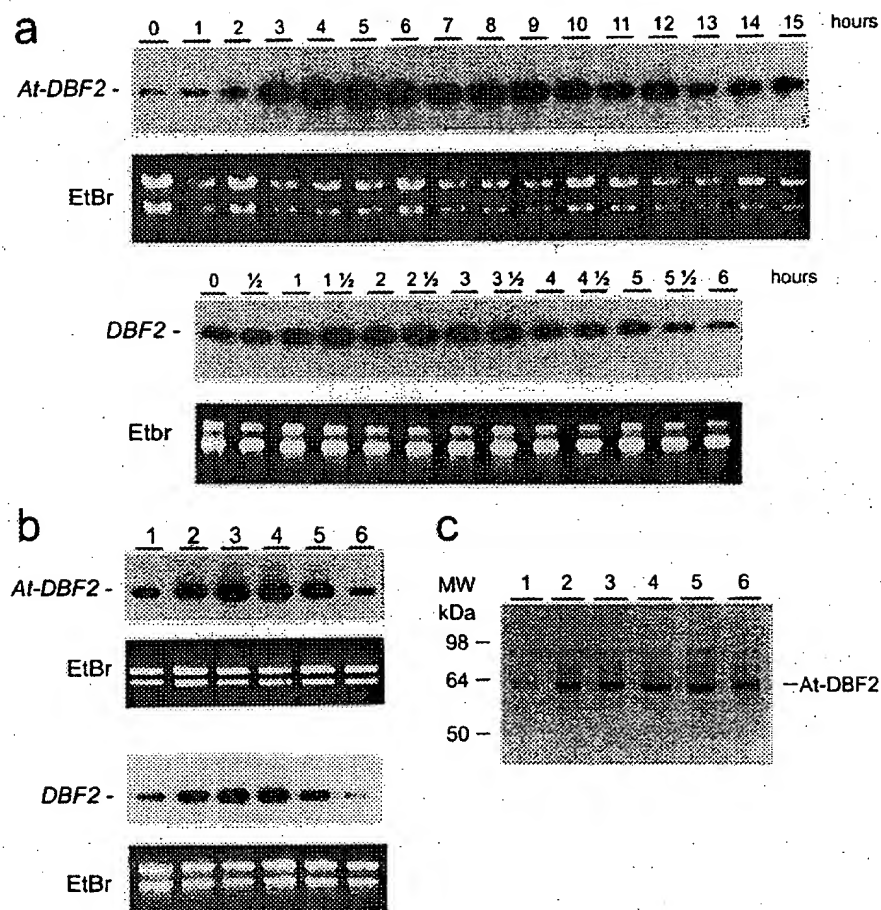


FIGURE 3



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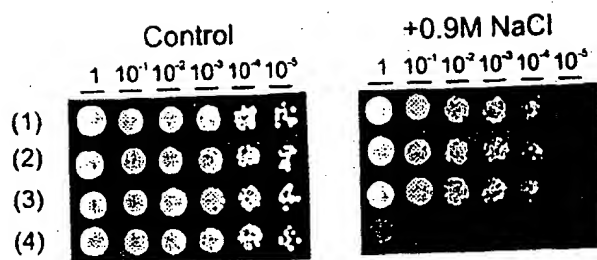


FIGURE 4

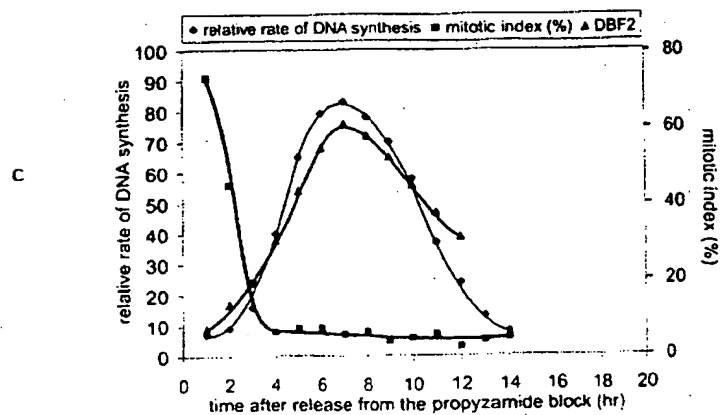
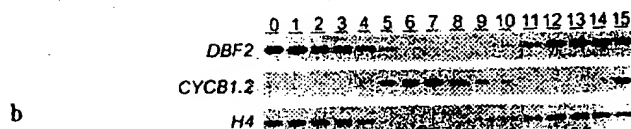
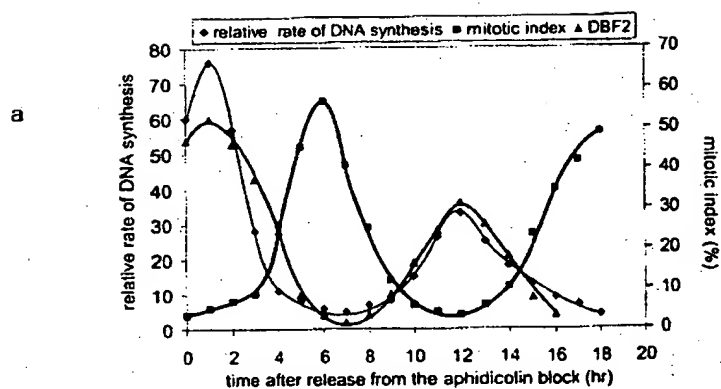


FIGURE 5

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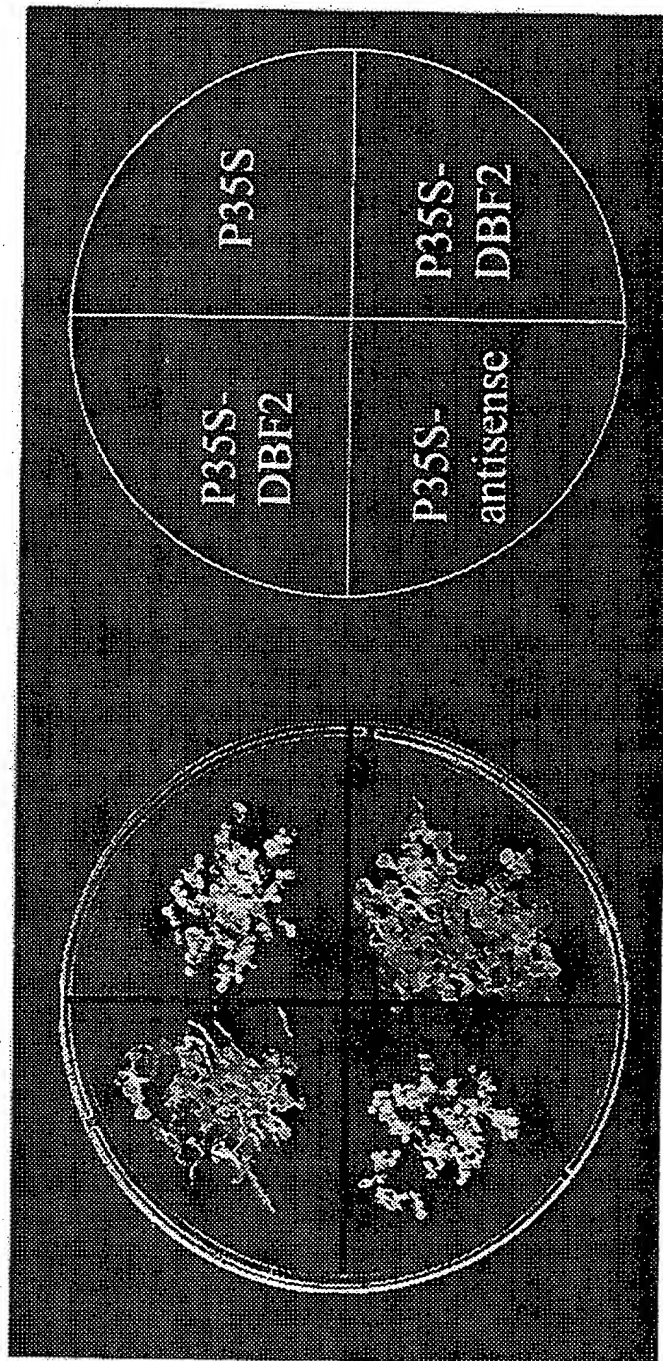


FIGURE 6

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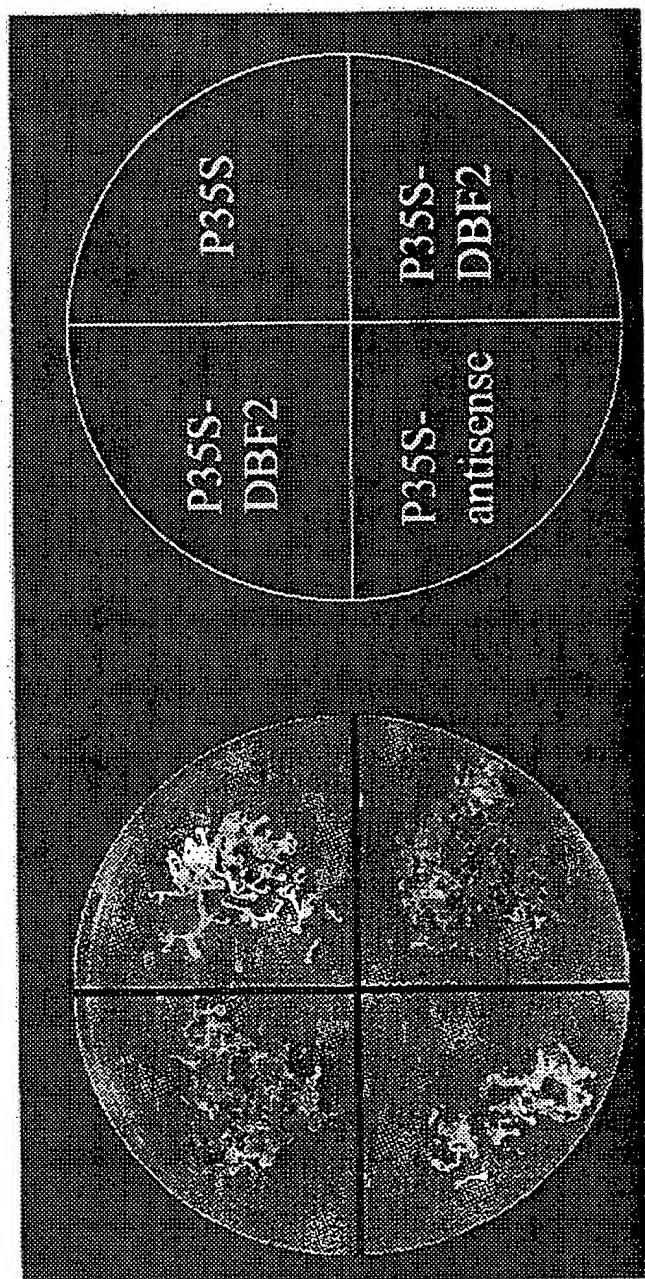


FIGURE 7

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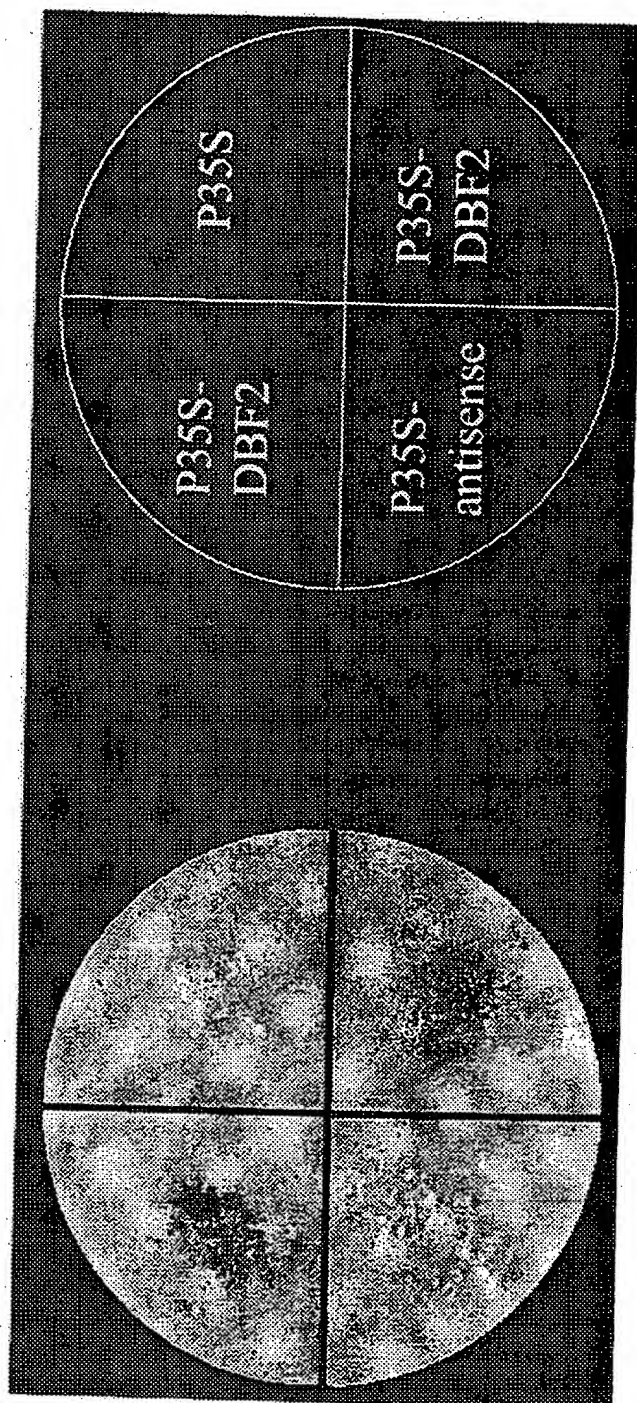


FIGURE 8

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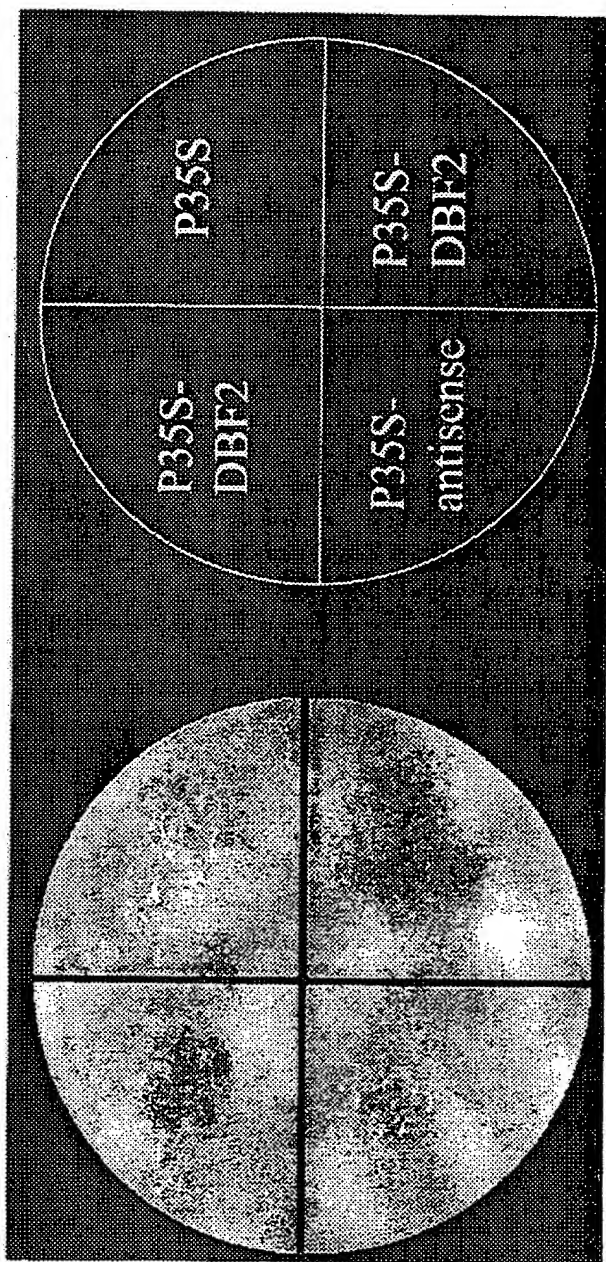


FIGURE 9

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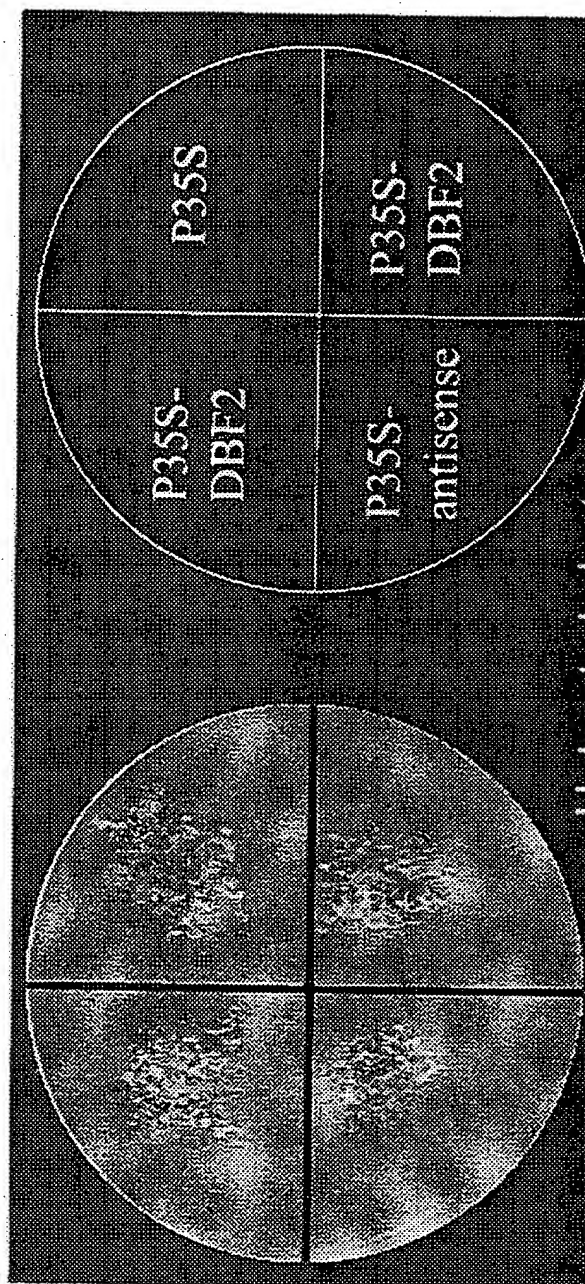


FIGURE 10



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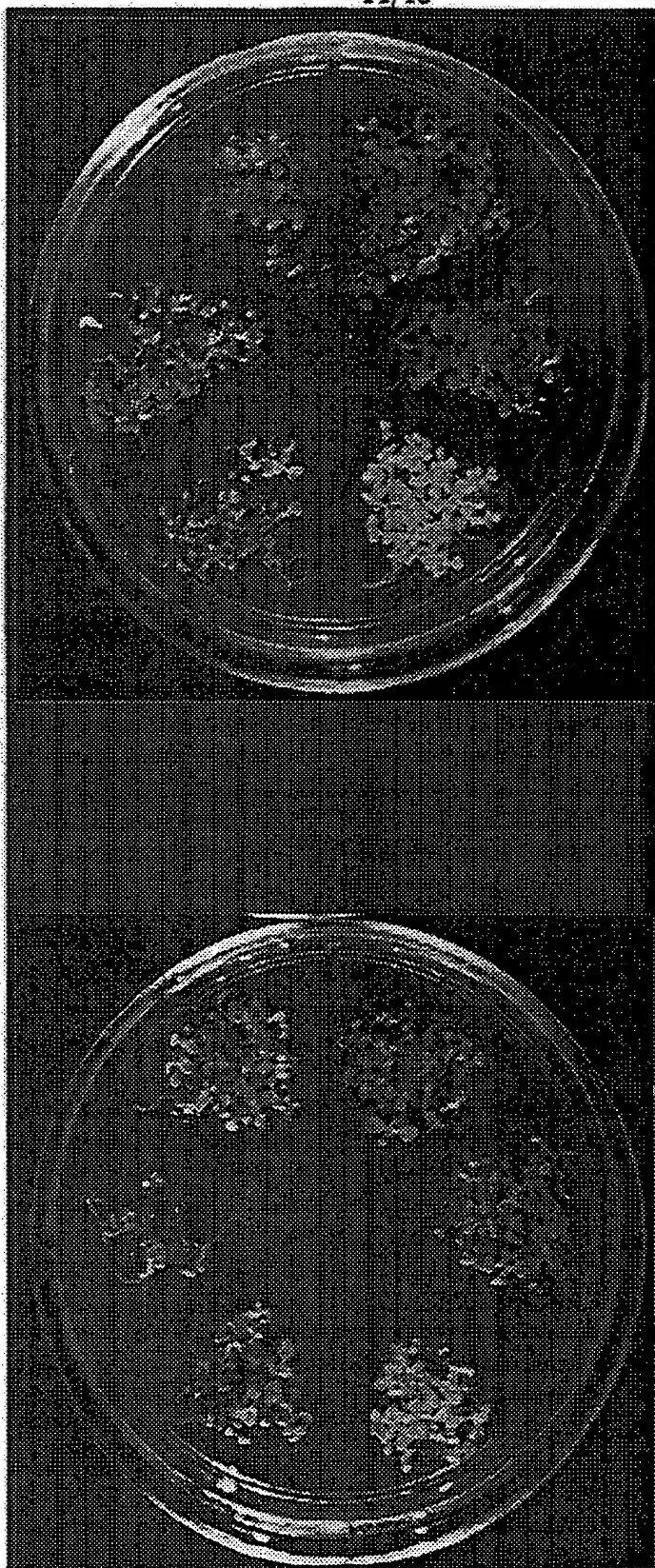


FIGURE 11

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FIGURE 12A

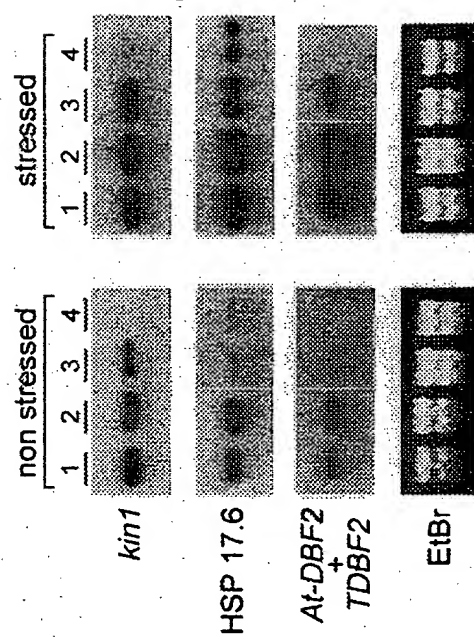


FIGURE 12c



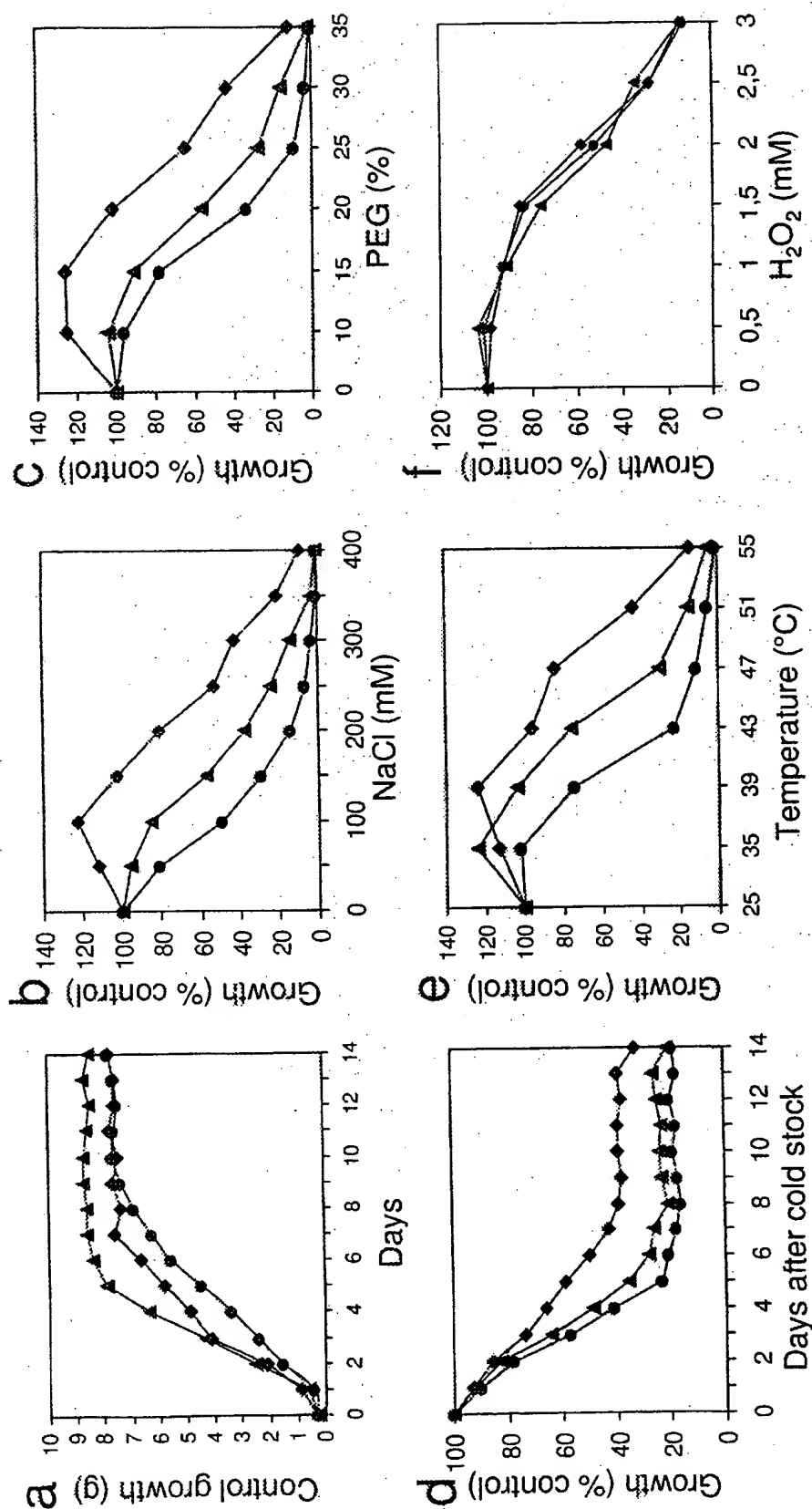


FIGURE 12B

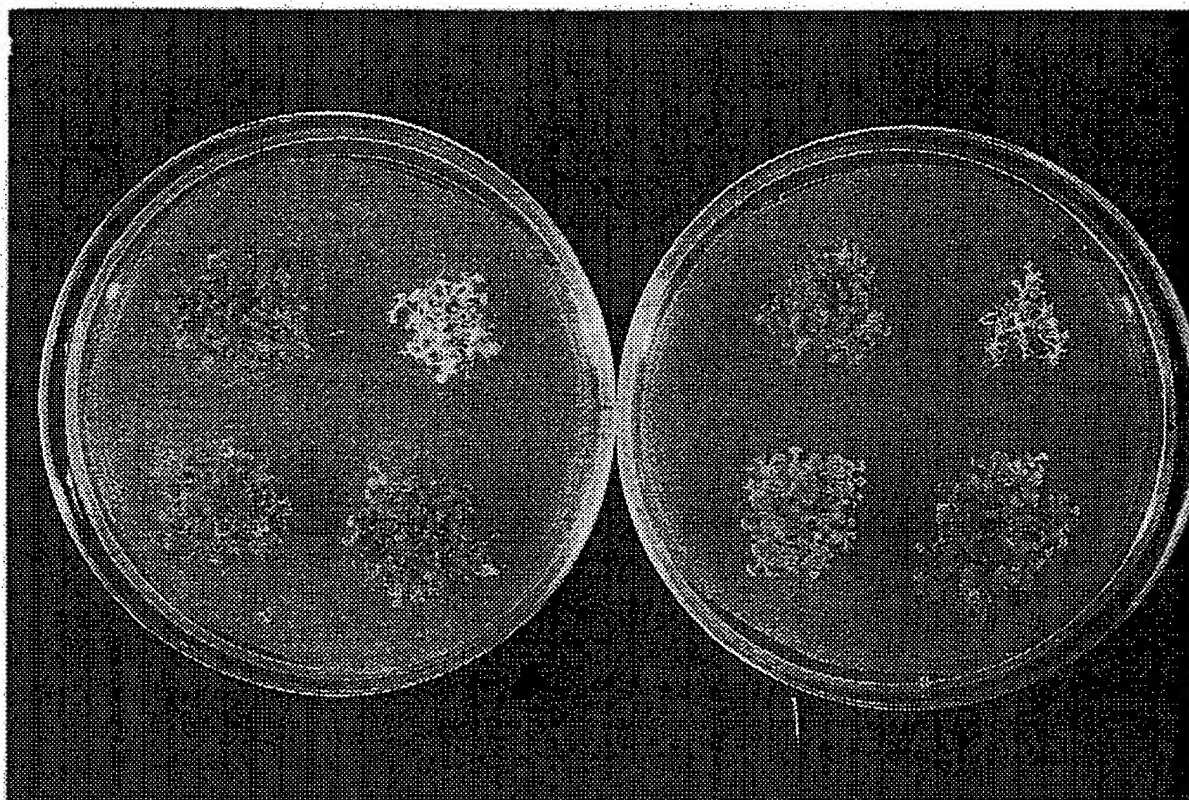


FIGURE 13

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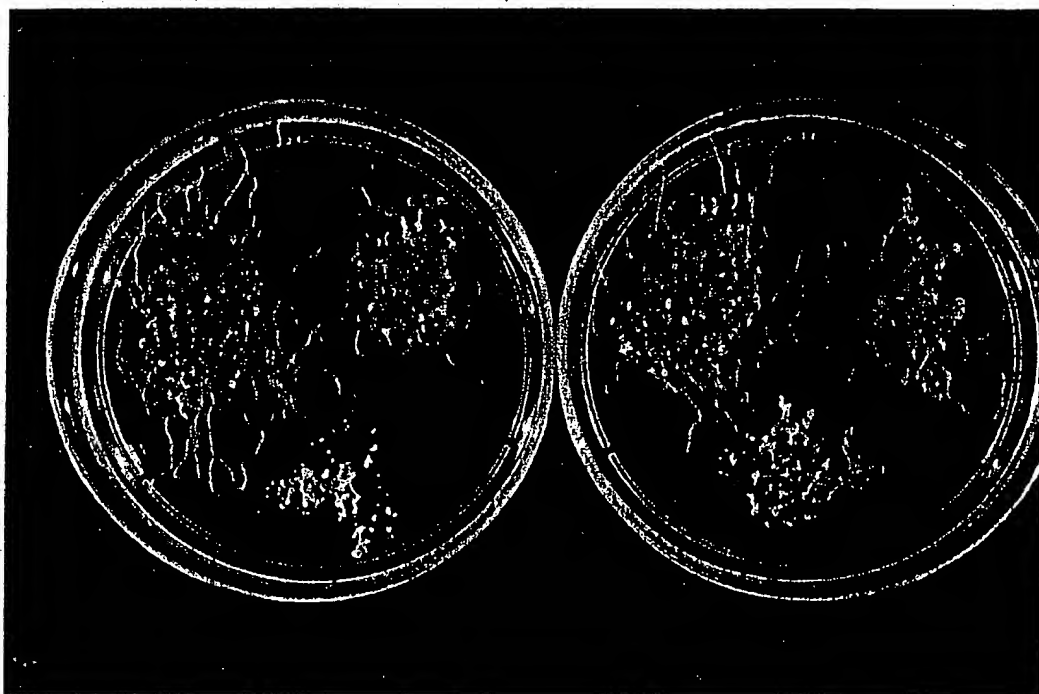


FIGURE 14

## SEQUENCE LISTING

&lt;110&gt; VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE

&lt;120&gt; Genes involved in tolerance to environmental stress

&lt;130&gt; VIB-14-NV/OSMO

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; 98202634.6

&lt;151&gt; 1998-08-04

&lt;160&gt; 126

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1909

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (40)..(1626)

&lt;400&gt; 1

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                                         Met Ala Gly Asn Met
                                         1           5

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Ser Cys Leu Ser Thr Asp Gly His Gly Thr Pro Gly Gly Ser Gly His
              10              15              20

ttc ccc aat cag aac cta acg aaa aga aga acg cgt cca gcg ggt atc      150
Phe Pro Asn Gln Asn Leu Thr Lys Arg Arg Thr Arg Pro Ala Gly Ile
              25              30              35

aac gac tcg cct tcg ccg gtg aaa tgc ttt ttt ttc ccc tat gaa gac      198
Asn Asp Ser Pro Ser Pro Val Lys Cys Phe Phe Phe Pro Tyr Glu Asp
              40              45              50

acc tcc aac acg tca tta aag gaa gtg tcc cag ccc acg aaa tac agt      246
Thr Ser Asn Thr Ser Leu Lys Glu Val Ser Gln Pro Thr Lys Tyr Ser
              55              60              65

tcc aat tcc cct cca gtc agc ccg gca att ttt tat gag agg gcg acg      294
Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe Tyr Glu Arg Ala Thr
              70              75              80              85

tcg tgg tgc acg caa agg gtg gtg agt ggg agg gca atg tac ttt cta      342
Ser Trp Cys Thr Gln Arg Val Val Ser Gly Arg Ala Met Tyr Phe Leu
              90              95              100

gaa tat tat tgc gat atg ttc gat tat gta att agc agg aga caa cgc      390

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Thr Lys Gln Val Leu Glu Tyr Leu Gln Gln Ser Gln Leu Pro Asn	
120 125 130	
tct gac cag atc aag ctc aac gaa gag tgg tcc tcc tat tta cag aga	486
Ser Asp Gln Ile Lys Leu Asn Glu Glu Trp Ser Ser Tyr Leu Gln Arg	
135 140 145	
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Glu His Gln Val Leu Ser Lys Arg Arg Leu Lys Pro Lys Asn Arg Asp	
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Phe Glu Met Ile Thr Gln Val Gly Gln Gly Tyr Gly His Val Tyr	
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Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys Ala Leu Lys Ile Leu	
185 190 195	
aat aag aag cta ggt ttc aaa ctt aat ggt aca tgc cat gtt ttg acc	678
Asn Lys Lys Leu Gly Phe Lys Leu Asn Gly Thr Cys His Val Leu Thr	
200 205 210	
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Glu Arg Gln Ser Leu Thr Thr Arg Ser Glu Thr Met Val Lys Leu	
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Leu Ser Gly Thr Thr Pro Val Gly Ser Arg Gly Met Ala Ile Glu Ser	
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Glu Leu Gly Gly Asp Phe Arg Thr Glu Ser Ile Gly Arg Arg Cys Leu	
250 255 260	
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Lys Ser Gly His Ala Arg Phe Tyr Ile Ser Glu Met Phe Cys Ala Val	
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Asn Glu Lys His Leu Leu Ser Lys Thr Asp Ser Thr Ile Ser Asn Glu	
280 285 290	
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Glu Asp Ser Ser Ile Asn Ile Arg Leu Glu Lys Phe Lys Asp Leu Gly	
295 300 305	
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Tyr Pro Ala Leu Ser Glu Lys Ser Ile Glu Asp Arg Arg Lys Leu Tyr	
310 315 320 325	
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Val Leu Arg Gly Lys Arg Tyr Glu Tyr	Thr Val Asp Tyr Trp Ser Leu		
345	350	355	
ggt tgt atg ctg ttt gag agc ttg gtc ggc tac acc ccc ttc agt ggc	1158		
Gly Cys Met Leu Phe Glu Ser Leu Val Gly Tyr Thr Pro Phe Ser Gly			
360	365	370	
tgc tgc acc aac gaa acg tat gcg atc agt cgt agc tgg aaa cag acg	1206		
Ser Ser Thr Asn Glu Thr Tyr Ala Ile Ser Arg Ser Trp Lys Gln Thr			
375	380	385	
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Leu Asn Arg Ala Arg His Glu Asp Gly Arg Ala Ala Phe Tyr Asn Arg			
390	395	400	
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Thr Trp Asp Leu Ile Thr Arg His Arg Ala Asp Leu Ser Thr Arg Thr			
410	415	420	
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Arg Ser Phe Glu His Glu Val Lys Met Ser Tyr Phe Ala Asp Ile Leu			
425	430	435	
ttt aag gcc tta aga tgc ata att cca cct ttc aca ccc caa cta gac	1398		
Phe Lys Ala Leu Arg Ser Ile Ile Pro Pro Phe Thr Pro Gln Leu Asp			
440	445	450	
agc gag acc gat gcc ggt tat ttc gat gac ttt tgg aat gag gct gac	1446		
Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe Trp Asn Glu Ala Asp			
455	460	465	
ata gcc aaa tac gct gac gtc ttt aat agt cag tgc tgc cgt acg gct	1494		
Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln Cys Cys Arg Thr Ala			
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cga cac aga aat ggt aaa cag ggt tcc agt ggt atg tta ttc aac ggg	1590		
Arg His Arg Asn Gly Lys Gln Gly Ser Ser Gly Met Leu Phe Asn Gly			
505	510	515	
cta gaa cac tca gac ccc ttc tca acc ttt tac tag taatcgccag	1636		
Leu Glu His Ser Asp Pro Phe Ser Thr Phe Tyr			
520	525		
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Tyr Gly His Val Tyr Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys  
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Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser  
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210 215 220

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Gln Ala Asn Ser Arg Leu Glu Asp Gln Ser Gln Val Phe Thr Ser Ser	
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Ser Arg Phe Val Asn Arg His Leu Phe Pro Tyr Met His L	
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Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro Asp Asp Ser Gln Ile	
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Thr Pro Arg Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser Arg			
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Asn Asp Lys Ap Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly			
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Ile Asp Leu Pe Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu r			
	385	390	395u
Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp Lys Lys Asp Glu			
	400	405	410
Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly Leu His Ser Arg			
	415	420	425
Lys Ser Ile Val Glu Asn Val Lys Arg Phe Leu Lys Asp Glu Trp Asn			
	430	435	440
Tyr Leu Asn Gln Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys			

445                      450                      455                      460  
 Val Trp Lys Asn Leu Pro Arg Arg Ile Ser Glu Ala Val Val Gln Val  
                                  465                      470                      475  
 Pro Gln Gln Lys Asn Asp Phe Asp Cys Gly Pro Phe Val Leu Phe Phe  
                                  480                      485                      490  
 Ile Lys Arg Phe Ile Glu Glu Ala Pro Gln Arg Leu Lys Arg Lys Asp  
                                  495                      500                      505  
 Leu Gly Met Phe Asp Lys Lys Trp Phe Arg Pro Asp Glu Ala Ser Ala  
                                  510                      515                      520  
 Leu Arg Ile Lys Ile Arg Asn Thr Leu Ile Glu Leu Phe Arg Val Ser  
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 Asp Gln Thr Glu

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 ggc act cgc ttg aga cca ttg act ctc agt ttc cca aag ccc ctt gtt 99  
 Gly Thr Arg Leu Arg Pro Leu Thr Leu Ser Phe Pro Lys Pro Leu Val  
                                  15                      20                      25  
 gat ttt gct aat aaa ccc atg atc ctt cat cag ata gag gct ctt aag 147  
 Asp Phe Ala Asn Lys Pro Met Ile Leu His Gln Ile Glu Ala Leu Lys  
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 gca gtt gga gtt gat gaa gtg gtt ttg gcc atc aat tat cag cca gag 195  
 Ala Val Gly Val Asp Glu Val Val Leu Ala Ile Asn Tyr Gln Pro Glu  
                                  45                      50                      55  
 gtg atg ctg aac ttc ttg aag gac ttt gag acc aag ctg gaa atc aaa 243  
 Val Met Leu Asn Phe Leu Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys  
                                  60                      65                      70  
 atc act tgc tca caa gag acc gag cca cta ggt acc gct ggt cct ctg 291  
 Ile Thr Cys Ser Gln Glu Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu  
                                  75                      80                      85                      90  
 gct cta gcg aga gac aaa ttg ctt gat gga tct gga gag ccc ttc ttt 339  
 Ala Leu Ala Arg Asp Lys Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe

95										100										105									
gtt	ctt	aac	agt	gat	gtg	att	agt	gag	tac	cct	ctt	aaa	gaa	atg	ctt	387													
Val	Leu	Asn	Ser	Asp	Val	Ile	Ser	Glu	Tyr	Pro	Leu	Lys	Glu	Met	Leu														
		110						115					120																
gag	ttt	cac	aaa	tct	cac	ggg	ggg	gaa	gcc	tcc	ata	atg	gta	aca	aag	435													
Glu	Phe	His	Lys	Ser	His	Gly	Gly	Glu	Ala	Ser	Ile	Met	Val	Thr	Lys														
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Val	Asp	Glu	Pro	Ser	Lys	Tyr	Gly	Val	Val	Val	Met	Glu	Glu	Ser	Thr														
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gga	aga	gtg	gag	aag	ttt	gtg	gaa	aag	cca	aaa	ctg	tat	gta	ggg	aac	531													
Gly	Arg	Val	Glu	Lys	Phe	Val	Glu	Lys	Pro	Lys	Leu	Tyr	Val	Gly	Asn														
155					160				165						170														
aag	atc	aac	gct	ggg	att	tat	ctt	ctg	aac	cca	tct	gtt	ctt	gat	aag	579													
Lys	Ile	Asn	Ala	Gly	Ile	Tyr	Leu	Leu	Asn	Pro	Ser	Val	Leu	Asp	Lys														
				175					180					185															
att	gag	cta	aga	ccg	act	tca	atc	gaa	aaa	gag	act	ttc	cct	aag	att	627													
Ile	Glu	Leu	Arg	Pro	Thr	Ser	Ile	Glu	Lys	Glu	Thr	Phe	Pro	Lys	Ile														
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gca	gca	gcg	caa	ggg	ctc	tat	gct	atg	gtg	cta	cca	ggg	ttt	tgg	atg	675													
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Asp	Ile	Gly	Gln	Pro	Arg	Asp	Tyr	Ile	Thr	Gly	Leu	Arg	Leu	Tyr	Leu														
	220					225					230																		
gac	tcc	ctt	agg	aag	aaa	tct	cct	gcc	aaa	tta	acc	agt	ggg	cca	cac	771													
Asp	Ser	Leu	Arg	Lys	Lys	Ser	Pro	Ala	Lys	Leu	Thr	Ser	Gly	Pro	His														
235					240				245				250																
ata	gtt	ggg	aat	gtt	ctt	gtt	gac	gaa	acc	gct	aca	att	ggg	gaa	gga	819													
Ile	Val	Gly	Asn	Val	Leu	Val	Asp	Glu	Thr	Ala	Thr	Ile	Gly	Glu	Gly														
			255					260					265																
tgt	ttg	att	gga	cca	gac	gtt	gcc	att	ggg	cca	ggc	tgc	att	gtt	gag	867													
Cys	Leu	Ile	Gly	Pro	Asp	Val	Ala	Ile	Gly	Pro	Gly	Cys	Ile	Val	Glu														
			270					275					280																
tca	gga	gtc	aga	ctc	tcc	cga	tgc	acg	gtc	atg	cgt	gga	gtc	cgc	atc	915													
Ser	Gly	Val	Arg	Leu	Ser	Arg	Cys	Thr	Val	Met	Arg	Gly	Val	Arg	Ile														
		285					290					295																	
aag	aag	cat	gcg	tgt	atc	tcg	agc	agt	atc	atc	ggg	tgg	cac	tca	acg	963													
Lys	Lys	His	Ala	Cys	Ile	Ser	Ser	Ser	Ile	Ile	Gly	Trp	His	Ser	Thr														
	300					305					310																		
gtt	ggg	caa	tgg	gcc	agg	atc	gag	aac	atg	acg	atc	ctc	ggg	gag	gat	1011													
Val	Gly	Gln	Trp	Ala	Arg	Ile	Glu	Asn	Met	Thr	Ile	Leu	Gly	Glu	Asp														
315					320					325					330														

gtt cat gtg agc gat gag atc tat agc aat gga gga gtt gtt ttg cca 1059  
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 335 340 345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga 1107  
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aa 1109

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<211> 361

<212> PRT

<213> Arabidopsis thaliana

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Met Ile Leu His Gln Ile Glu Ala Leu Lys Ala Val Gly Val Asp Glu  
 35 40 45

Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu  
 50 55 60

Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys Ile Thr Cys Ser Gln Glu  
 65 70 75 80

Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Lys  
 85 90 95

Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe Val Leu Asn Ser Asp Val  
 100 105 110

Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu Glu Phe His Lys Ser His  
 115 120 125

Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys  
 130 135 140

Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe  
 145 150 155 160

Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile  
 165 170 175

Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr  
 180 185 190

Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile Ala Ala Ala Gln Gly Leu  
 195 200 205

Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg  
 210 215 220  
 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys  
 225 230 235 240  
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu  
 245 250 255  
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp  
 260 265 270  
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser  
 275 280 285  
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile  
 290 295 300  
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg  
 305 310 315 320  
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu  
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 cct tat cga acc aac tct tct ttc ggc tca aag tca tcg ctt ctc ttt 98  
 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe  
 15 20 25 30  
 cgg tct cca tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146  
 Arg Ser Pro Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly  
 35 40 45  
 aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194  
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys  
 50 55 60

gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
65 70 75	
tggt gga gat cat atg cat cat ggc ttt tat gac cct gat tct tct gtt	290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag	386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga	434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
130 135 140	
tat ctt gcc tct aaa ttt gga gct gaa tgc att ggc att act ctc agc	482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	



tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca 914  
 Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala  
 290 295 300

tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt 962  
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 305 310 315

att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010  
 Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys  
 320 325 330

ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055  
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 35 40 45

Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile  
 50 55 60

Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly  
 65 70 75 80

Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu  
 85 90 95

Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser  
 100 105 110

Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys  
 115 120 125

Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu  
 130 135 140

Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val  
 145 150 155 160

Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His  
 165 170 175

Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp  
 180 185 190  
 Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro  
 195 200 205  
 Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly  
 210 215 220  
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly  
 225 230 235 240  
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys  
 245 250 255  
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn  
 260 265 270  
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser  
 275 280 285  
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr  
 290 295 300  
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys  
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 ctc gag atc gac gat gac cag aaa cta cgt gcg ttt tac gac aag aga 95  
 Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg  
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 atc tct caa gaa gtc agt gga gat gct ttg gcc gag gag ttc aaa gga 143  
 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly  
 35 40 45

tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg 191  
 Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met  
 50 55 60

aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga 239  
 Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg  
 65 70 75

gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga 287  
 Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg  
 80 85 90 95

aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg 335  
 Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu  
 100 105 110

aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc 383  
 Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr  
 115 120 125

gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt 431  
 Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg  
 130 135 140

aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac 479  
 Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn  
 145 150 155

act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa 527  
 Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys  
 160 165 170 175

gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag 575  
 Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys  
 180 185 190

aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct 623  
 Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser  
 195 200 205

gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag 671  
 Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln  
 210 215 220

cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct 719  
 Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser  
 225 230 235

tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca 768  
 Ser Ala Ala Ala Lys Pro Ser Val Thr Ala  
 240 245 250

&lt;210&gt; 28

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 28

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Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr
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Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys
      50           55           60

Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
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Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg
      85           90           95

Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
      100          105          110

Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
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His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys
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Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr
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Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala
      165          170          175

Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg
      180          185          190

Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp
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Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg
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Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser Ser
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Ala Ala Ala Lys Pro Ser Val Thr Ala
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 ctcttctctt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167  
 Thr Glu Lys Ala Phe Leu Lys  
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cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217  
 Gln Pro Lys Val Phe Leu Se  
 15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277  
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 r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly  
 20 25 30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373  
 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu  
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gcc att gat g gtatgtttta gcttttaact cgttataata gataaggaac 423  
 Ala Ile Asp G  
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tcttggttg ttgtgttcac atagtcgata gatttcaaat gctattttgt cttgtagaat 483  
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 Gly Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg  
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 Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly  
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 Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala  
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 Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val  
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 Lys Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His  
                     100                    105                    110  
 Val Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly  
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 Gln Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val  
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 Lys Glu Glu Ala Pro Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly  
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Thr	Gly	Lys	Pro	Pro	Trp	Ser	Glu	Gln	Tyr	Gln	Gln	Phe	Ala	Ala	Val	
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ctt	cat	att	ggt	aga	aca	aaa	gct	cat	cct	cca	att	cca	gaa	gac	ctc	916
Leu	His	Ile	Gly	Arg	Thr	Lys	Ala	His	Pro	Pro	Ile	Pro	Glu	Asp	Leu	
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Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile	350	355	360	
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Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn	380	385	390	395
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atg ccc cct cct aag atg ctt cca cca acg gca agg gat tca gta gca	48
Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala	
1 5 10 15	
ggg aca ggg ggt agt cca cca cct cca cct cca cca cca gct cgg tgg	96
Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp	
20 25 30	
agg gta gcg ggg gag gga gga ttg gat aca aca cca ccg ccg ccc cct	144
Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro	
35 40 45	
cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg	192
Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala	
50 55 60	
ccc cct cct cgt cag cct cca cgt cct cca aca gca ccg tgg tca gcg	240
Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala	
65 70 75 80	
atg ggc aga gtg atg tgc agt ccg ccg ata cca cta tcg cgg agt aga	288
Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg	
85 90 95	
cta gcg ctt gac gac caa cgt tgg ccg gat tgg aca acg aac ggt tgg	336
Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp	
100 105 110	
cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa	384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln	
115 120 125	
ggg gcc cga cga tcc tca gtg tca cca gcg ccg gtg aca acg ggg atg	432
Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met	
130 135 140	
gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc	480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg	
145 150 155 160	
gac tgg acg agg aaa cga atg gtc agg aaa ttg ctt aaa gca agg gcg	528
Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala	
165 170 175	
aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg	576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val	
180 185 190	
ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac	624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn	
195 200 205	
ttg aaa ttc acg tgc ccg agg gat gtg gca ata gcc acg ttc agc ggc	672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly	

210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc			720
Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser			
225	230	235	240
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata			768
Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile			
	245	250	255
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc			816
Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr			
	260	265	270
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc			864
Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val			
	275	280	285
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa			912
Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu			
	290	295	300
ggg gga tgg cgg tat gcg gca ctc gag gag cat aag acg gag ccg gga			960
Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly			
305	310	315	320
cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggg			1008
Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly			
	325	330	335
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggg gca			1056
Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala			
	340	345	350
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc			1104
Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile			
	355	360	365
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg			1152
Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala			
	370	375	380
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac			1200
Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn			
385	390	395	400
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga			1248
Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg			
	405	410	415
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg			1296
Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr			
	420	425	430
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg			1344
Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr			
	435	440	445

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gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392
Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
  450          455          460

gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440
Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
465          470          475          480

agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488
Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
          485          490          495

gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536
Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
          500          505          510

ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584
Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
          515          520          525

gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635
Gly Arg Arg Trp Arg Glu
  530          535

tggaccggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695

taaaaaaaaa caacaaaaaaaa aaaaaaaaaac aaaaaaaaaa a 1736

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&lt;210&gt; 36

&lt;211&gt; 534

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 36

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Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala
  1          5          10          15

Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp
          20          25          30

Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro
          35          40          45

Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
          50          55          60

Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
          65          70          75          80

Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
          85          90          95

Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
          100          105          110

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Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln  
 115 120 125  
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met  
 130 135 140  
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg  
 145 150 155 160  
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala  
 165 170 175  
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val  
 180 185 190  
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn  
 195 200 205  
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly  
 210 215 220  
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser  
 225 230 235 240  
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile  
 245 250 255  
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr  
 260 265 270  
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val  
 275 280 285  
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu  
 290 295 300  
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly  
 305 310 315 320  
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly  
 325 330 335  
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala  
 340 345 350  
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile  
 355 360 365  
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala  
 370 375 380  
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn  
 385 390 395 400  
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg  
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr  
 420 425 430  
 Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr  
 435 440 445  
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met  
 450 455 460  
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu  
 465 470 475 480  
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr  
 485 490 495  
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro  
 500 505 510  
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr  
 515 520 525  
 Gly Arg Arg Trp Arg Glu  
 530

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 <222> (374) .. (493)

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 Met Gln Val Ala Asp Ile Ser Leu Gln Gly Asp  
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 gct aag aag ggt gcc aac ctc ttc aag gtacgaacag agcaaagatg 97  
 Ala Lys Lys Gly Ala Asn Leu Phe Lys  
 15 20  
 ccgctgaaaa ttctcacggc gcattctatc ccgcagaact tttctgacca ctttgtag 155  
 acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203  
 Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys  
 25 30 35

att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251  
 Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val  
                     40                    45                    50

gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299  
 Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp  
                     55                    60                    65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354  
 Lys Asp Asp Thr Leu  
                     70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406  
                                     Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile  
   75                                    80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454  
 Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg  
                     85                    90                    95                    100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503  
 Asn Asp Leu Ile Thr Phe Leu Glu Glu Thr Lys  
                     105                    110

acccc 508

<210> 38  
 <211> 112  
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 <213> Arabidopsis thaliana

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                     20                    25                    30

Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys  
                     35                    40                    45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys  
                     50                    55                    60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro  
                     65                    70                    75                    80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys  
                     85                    90                    95

Pro Lys Asp Arg Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys  
                     100                    105                    110

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 Met Ala Pro Thr Pro Ser Ser Ser Arg Ser Asn Gln Thr Gln Tyr Thr  
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tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96  
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys  
 20 25 30

acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144  
 Thr Pro Asn Thr Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro  
 35 40 45



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gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192
Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys
    50                55                60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240
Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val
    65                70                75                80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288
Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe
                85                90                95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336
Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu
                100                105                110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384
Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr
                115                120                125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432
Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys
    130                135                140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct 480
Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser
    145                150                155                160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat 528
Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
                165                170                175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta 576
Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu
                180                185                190

ggt att ggt tgg cct aaa gga gca agc act aag gtaaagtttc ttgattgata 629
Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys
    195                200

actttagtat acattgaatt ggctttaaaag gtgtgtactt tggtgttttg ttacag gtg 688
Val
                205                210                215                220

ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa 784
Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys
                225                230                235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt 832
Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser
    240                245                250

cac tgc att gtaagaacga tcttcttgat tgatgtgat gcatagcttt 881

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His Cys Ile  
255

atgcagctta tctctgtttt aacttactag tgtggttgtt tctttttgta g atc ata 938  
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986  
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala  
260 265 270

ggc tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag 1034  
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys  
275 280 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090  
Met Gln  
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144  
Thr Ala Lys Ile Asn  
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192  
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly  
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240  
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln  
315 320 325

gtgaaattct tgttccattg ttttatcttc tggaaaatgt tttacgtgtt gcttggtttt 1300

cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat 1355  
Asp Ser Phe Glu Asp  
330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag 1403  
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys  
335 340 345

gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag 1451  
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys  
350 355 360 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt 1499  
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly  
370 375 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg 1547  
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met  
385 390 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa 1595  
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys  
400 405 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt 1643

Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val	
415 420 425	
gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat	1691
Ala Ala Leu Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn	
430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
450 455 460	
tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa	1787
Ser Glu Leu Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu	
465 470 475	
ttt gtt gag atg gag aga agg aga atg gag gaa agg ata gtt cag cag	1835
Phe Val Glu Met Glu Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
480 485 490	
caa gag gaa ctg gag atg atg agg aga cgg tta gag gaa atc gag gtt	1883
Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
495 500 505	
gag ttc cgc cgc tca aat gga gga agt gtt gat gaa act agt ggg ttt	1931
Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
510 515 520 525	
gcc aaa aga ctc agg agt ctt tac tct gat gat gat cct ggt atg gtg	1979
Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
530 535 540	
aag tca atg gac ctt gac atg ggt gat cca gaa cct gtc aag caa gtg	2027
Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
545 550 555	
tgg gga gct gtt tca cac caa tca agc aac act att agt agc aac ttc	2075
Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe	
560 565 570	
act aac ctt ttg caa ccg aag cct tca gag aat atg ctt aca cag atg	2123
Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met	
575 580 585	
tat cct gac cgg gta tgc ttg agc act gtc ttt gaa gaa gaa gaa gtt	2171
Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Glu Val	
590 595 600 605	
gaa gaa gag gaa gaa aaa gtg ata gtc gag gat aaa agc atc tgc ttg	2219
Glu Glu Glu Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu	
610 615 620	
ata aca aca cca atg cct agt ttg aac tct gaa ggt ttg ggt aaa gag	2267
Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu	
625 630 635	
aac tgc ttc aac ggt gca gat gac aag gaa tca gcc tcg tct aga agg	2315
Asn Cys Phe Asn Gly Ala Asp Asp Lys Glu Ser Ala Ser Ser Arg Arg	

640	645	650	
ttg aga att caa aac att ttc acc ctt tgt ggc aat cag aga gag ctg Leu Arg Ile Gln Asn Ile Phe Thr Leu Cys Gly Asn Gln Arg Glu Leu 655 660 665			2363
tct caa cac agt gga cag gag gag gat caa gcc aat att gca tca cct Ser Gln His Ser Gly Gln Glu Glu Asp Gln Ala Asn Ile Ala Ser Pro 670 675 680 685			2411
gat aag aaa gac aat cag ttc ttt tct att acg aat aag gcc gaa gca Asp Lys Lys Asp Asn Gln Phe Phe Ser Ile Thr Asn Lys Ala Glu Ala 690 695 700			2459
cta gca gta gaa gaa gca aag gaa aac aat atc tca gtc gat caa agg Leu Ala Val Glu Glu Ala Lys Glu Asn Asn Ile Ser Val Asp Gln Arg 705 710 715			2507
gaa aac ggt cag cta gat atc tat gtt aaa tgg gaa aca gct gct gat Glu Asn Gly Gln Leu Asp Ile Tyr Val Lys Trp Glu Thr Ala Ala Asp 720 725 730			2555
aac cct cga aag ctc ata aca aca ctg aga gtt aca aag gat gca aca Asn Pro Arg Lys Leu Ile Thr Thr Leu Arg Val Thr Lys Asp Ala Thr 735 740 745			2603
cta gct gac ttg agg aag ctt att gag atc tac ctt gga tct gat aat Leu Ala Asp Leu Arg Lys Leu Ile Glu Ile Tyr Leu Gly Ser Asp Asn 750 755 760 765			2651
cag gct ttt acc ttt ctc aag ctc ggg gta ata aac ttg aac caa caa Gln Ala Phe Thr Phe Leu Lys Leu Gly Val Ile Asn Leu Asn Gln Gln 770 775 780			2699
gca caa aaa gct ttt cat ttt tat ctg ttt gttatgctct gacctaataat Ala Gln Lys Ala Phe His Phe Tyr Leu Phe 785 790			2749
gcagttattt caatgtatga ag gaa cca tgt gga gct caa gtg gca aag gag Glu Pro Cys Gly Ala Gln Val Ala Lys Glu 795 800			2801
aaa gaa tca aca gtt caa gct acg agc cta cct ctc tgc aac gga cac Lys Glu Ser Thr Val Gln Ala Thr Ser Leu Pro Leu Cys Asn Gly His 805 810 815			2849
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Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala  
 100 105 110  
 Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met  
 115 120 125  
 Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala  
 130 135 140  
 Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val  
 145 150 155 160  
 Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg  
 165 170 175  
 Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val  
 180 185 190  
 His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp  
 195 200 205  
 Gly His Trp Asp Ile Phe Leu Asp Glu Asp Leu Glu Thr Ala Lys Lys  
 210 215 220  
 Ala Ile Glu Glu Glu Ala  
 225 230

<210> 45  
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 <212> DNA  
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<220>  
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 cct ata tcc tcc aca ctt aat cag cat tta gta gat tat cca acc ccg 98  
 Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro  
 15 20 25  
 agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt 146  
 Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys  
 30 35 40 45  
 tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca 194  
 Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr  
 50 55 60  
 cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat 242

Pro His Val Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp	
65 70 75	
ggt gaa ggg ggc tgg ttg ctc cgt tat atg cat gct aat ggg gca agt	290
Val Glu Gly Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser	
80 85 90	
atg ttt ctt att gtg gtt tac ctt cat att ttt cgt ggt cta tat cat	338
Met Phe Leu Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His	
95 100 105	
gcg agt tat agc agt cct agg gaa ttt gtt tgg tgt ctt gga gtt gta	386
Ala Ser Tyr Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val	
110 115 120 125	
atc ttc cta tta atg att gtg aca gct ttt ata gga tat gta cta cct	434
Ile Phe Leu Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro	
130 135 140	
tgg ggt cag atg agc ttt tgg gga gct aca gta att aca agc tta gct	482
Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala	
145 150 155	
agc gcc ata cct gta gta gga gat acc ata gtg act tgg ctt tgg ggt	530
Ser Ala Ile Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly	
160 165 170	
ggt ttc tcc gtg gac aat gcc acc tta aat cgt ttt ttt agt ctt cat	578
Gly Phe Ser Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His	
175 180 185	
cat tta ctc ccc ttt att tta gta ggc gcc agt ctt ctt cat ctg gcc	626
His Leu Leu Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala	
190 195 200 205	
gca ttg cat caa tat gga tca aat aat cca ttg ggt gta cat tct gag	674
Ala Leu His Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu	
210 215 220	
atg gat aaa ata gct ttt tac cct tat ttt tat gtc aag gat cta gtt	722
Met Asp Lys Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val	
225 230 235	
ggt tgg gta gct ttt gct atc ttt ttt tct att tgg att ttt tat gct	770
Gly Trp Val Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala	
240 245 250	
cct aat gtt ttg gga cat ccc gac aat tat ata cct gct aat ccg atg	818
Pro Asn Val Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met	
255 260 265	
tcc acc ccg cct cat att gtg ccg gaa tgg tat ttc cta ccg atc cat	866
Ser Thr Pro Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His	
270 275 280 285	
gcc att ctt cgt agt ata cct gac aaa gcg gga ggt gta gcc gca ata	914
Ala Ile Leu Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile	

290	295	300	
gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg			962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met			
305	310	315	
tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg			1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp			
320	325	330	
ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct			1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro			
335	340	345	
gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc			1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe			
350	355	360	365
ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga			1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly			
370	375	380	
att cct aat tct tac acg gat gag act gat cac acc tga tcagtga			1203
Ile Pro Asn Ser Tyr Thr Asp Glu Thr Asp His Thr			
385	390		

&lt;210&gt; 46

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 46

Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln Pro Ile Ser			
1	5	10	15
Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro Ser Asn Leu			
20	25	30	
Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile			
35	40	45	
Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val			
50	55	60	
Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly			
65	70	75	80
Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu			
85	90	95	
Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr			
100	105	110	
Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu			
115	120	125	

Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln  
 130 135 140  
 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile  
 145 150 155 160  
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser  
 165 170 175  
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu  
 180 185 190  
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His  
 195 200 205  
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys  
 210 215 220  
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val  
 225 230 235 240  
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val  
 245 250 255  
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro  
 260 265 270  
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu  
 275 280 285  
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val  
 290 295 300  
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg  
 305 310 315 320  
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu  
 325 330 335  
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala  
 340 345 350  
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe  
 355 360 365  
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn  
 370 375 380  
 Ser Tyr Thr Asp Glu Thr Asp His Thr  
 385 390

&lt;210&gt; 47

&lt;211&gt; 1194

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1194)

&lt;400&gt; 47

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Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe	
1 5 10 15	
cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg	96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro	
20 25 30	
caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt	144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	
35 40 45	
aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt	192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	
50 55 60	
att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt	240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	
65 70 75 80	
tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc	288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	
85 90 95	
aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc	336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	
100 105 110	
act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc	384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	
115 120 125	
gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat	432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	
130 135 140	
aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct	480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	
145 150 155 160	
agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg	528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	
165 170 175	
acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca	576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	
180 185 190	
gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att	624
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	
195 200 205	



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cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
210 215 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
290 295 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
325 330 335

ggt gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
370 375 380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga 1194
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385 390 395

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&lt;210&gt; 48

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 48

Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe

1	5	10	15
Arg Gly Asn Tyr	Ala Ala Thr Leu Asp Val	Ser Tyr Pro Val	Phe Pro
20	25	30	
Gln Asn Lys Asp	Gly Arg Ala Leu Gln Lys Val	Leu Gly Thr Ile	Arg
35	40	45	
Asn Gly Asp Leu	Ala Val Ser Ala Pro Lys Thr	Ser Leu Arg Ala	Gly
50	55	60	
Ile Phe Gly Glu	Gly Ser Ser Leu Val Asp Gln Met	Pro Cys Lys Val	
65	70	75	80
Tyr Val Ala Phe	His Lys Glu Ser Tyr Cys Ser	Leu Thr Gly Leu	Ser
85	90	95	
Lys Arg Gly Val	Ala Ile Asn Glu Ala Ser Leu	Ser Leu Val Gly	Ile
100	105	110	
Thr Lys Val Arg	Ala Pro Val Gly Asn Thr Val	Gly Ala Glu Ala	Thr
115	120	125	
Val Tyr Ile Gly	Ser Pro Lys Pro Tyr Thr Glu	Cys Ser Thr Pro	Asn
130	135	140	
Lys Met Tyr Ala	Val Ala Ala Gly Phe Lys Val	Ala Ser Phe Ala	Ala
145	150	155	160
Ser Thr Cys Val	Arg Pro Pro Ala Arg Ala Arg	Arg Thr Leu Thr	Val
165	170	175	
Thr Ser Thr Val	Thr Leu Ser Met Ala Thr Gly	Lys Cys Val Asn	Thr
180	185	190	
Gly Asn Glu Pro	Val Ser Lys Pro Thr Gly Val	Arg Met Met Leu	Ile
195	200	205	
Pro Leu Asp Ala	Thr Leu Ile Lys Val Trp Thr Gly	Glu Val Lys Lys	
210	215	220	
Ala Ile Val Ser	Arg Pro Ala Lys Ile Phe Asn	Ser Val Gly Asn	Leu
225	230	235	240
Glu Arg Pro Ser	Ile Ser His Ser Cys Gly Gln	Gly Leu Asp Glu	Ala
245	250	255	
Ala Ala Tyr Ile	Lys Gly Arg Leu Ser Pro Ile	Val Lys Ala Glu	Arg
260	265	270	
Ile Lys Val Leu	Val Lys Asp Glu His Glu Glu	Val Lys Glu Leu	Leu
275	280	285	
Gln Glu Gly Tyr	Glu Glu Ile Val Gly Glu Ser	Pro Ser Phe Asn	Leu
290	295	300	
Ala Gln Glu Ala	Trp Glu Lys Ala Glu Arg	Arg Ala Lys Gly	Gln Ser

305                      310                      315                      320  
 Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr  
                                  325                      330                      335  
 Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu  
                                  340                      345                      350  
 Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu  
                                  355                      360                      365  
 Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser  
                                  370                      375                      380  
 Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn  
                                  385                      390                      395

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          Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val  
                  1                      5                      10                      15  
 gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97  
 Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser  
                                  20                      25                      30  
 cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145  
 Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile  
                                  35                      40                      45  
 agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193  
 Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met  
                                  50                      55                      60  
 act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241  
 Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp  
                                  65                      70                      75  
 ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289  
 Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser  
                                  80                      85                      90                      95  
 tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337  
 Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu  
                                  100                      105                      110

gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385  
 Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile  
 115 120 125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433  
 Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val  
 130 135 140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481  
 Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg  
 145 150 155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529  
 Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr  
 160 165 170 175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577  
 Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln  
 180 185 190

gaa tca caa aaa gac gag ctt taa agcaaagtcc 611  
 Glu Ser Gln Lys Asp Glu Leu  
 195

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 <212> PRT  
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 20 25 30

Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser  
 35 40 45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr  
 50 55 60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu  
 65 70 75 80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys  
 85 90 95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala  
 100 105 110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe  
 115 120 125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys  
 130 135 140

Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro  
 145 150 155 160

Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala  
 165 170 175

Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu  
 180 185 190

Ser Gln Lys Asp Glu Leu  
 195

<210> 51  
 <211> 1398  
 <212> DNA  
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<220>  
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cca tgt aga ggc gcg tca atc act gga tct cta cgt gac cgt cga ccg 96  
 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro  
 20 25 30

acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144  
 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg  
 35 40 45

tgt ggc tct tgc ccc agt gtc gac cgt tgc gga cac gca agt gcc gcc 192  
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
 50 55 60

ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240  
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
 65 70 75 80

caa gag tac tgg tgc tcg act gaa ccg acc ctt gac tgg ggc ccc ggt 288  
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
 85 90 95

ggg gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336  
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu  
 100 105 110

att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384  
 Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys  
 115 120 125

gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt	432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
130 135 140	
att att att agg gag ggg ttg aaa act gat cct tta aaa tac act aag	480
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys	
145 150 155 160	
cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt	528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
165 170 175	
aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct	576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala	
180 185 190	
act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac	624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
195 200 205	
gga tgc cgc cac tca ctt tcg gat ggt ctc atg agg gct act gat gtt	672
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val	
210 215 220	
cgt cgc ccc tgc aag gta gcg ctt gta ggc ggt tac gga gat gtc ttt	720
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
225 230 235 240	
aag ggt tgg gtt gct gcc ttg aag caa gct ggt gca cgt gtc atc gtg	768
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
245 250 255	
act gag atc ccg caa atc tgt gcc gtc caa gct acc atg gaa ggt agt	816
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
260 265 270	
tcg gtc ctt acc ctt gag gat gtc gtt tca gat gtt gat cgc ttc gtt	864
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
275 280 285	
acg aca acc ggt aac aag gac ctc atc atg gtt gac cac atg agg cga	912
Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
290 295 300	
atg aag aac cag gcc ata gtt tgc aac att cga cgt ttc gac aat gaa	960
Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu	
305 310 315 320	
atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca	1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
325 330 335	
atc aag gcc cag act gac aga tgg gtc ttt cgc gac acc aac aga ggt	1056
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
340 345 350	
atc att gtc cca gcc gag ggg cgt ctc atg acg atg gga tgc gcc act	1104

Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr  
 355 360 365

gga cac ccc agc ttc cgg acg tcc tgc tct ttc act aac caa gtc agt 1152  
 Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser  
 370 375 380

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 Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys  
 385 390 395 400

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 Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu  
 405 410 415

cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296  
 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr  
 420 425 430

ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac 1344  
 Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His  
 435 440 445

cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392  
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 35 40 45

Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
 50 55 60

Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
 65 70 75 80

Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
 85 90 95

Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

109



405					410					415					
His	Leu	Val	Lys	Leu	Gly	Ala	Arg	Leu	Thr	Lys	Leu	Ser	Arg	Cys	Thr
420					425					430					
Leu	Leu	Cys	Thr	Asp	Asp	Pro	Val	Glu	Gly	Arg	Lys	Glu	Pro	Pro	His
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gac	gtc	gat	gaa	att	gtc	agg	tta	agg	aag	agg	ttt	ttc	aag	ttg	gac	96	
Asp	Val	Asp	Glu	Ile	Val	Arg	Leu	Arg	Lys	Arg	Phe	Phe	Lys	Leu	Asp		
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Arg	Asp	Cys	Ser	Gly	Ser	Glu	Leu	Gly	Ser	Glu	Phe	Met	Ser	Leu	Pro		
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caa	gtt	agt	tcg	aac	cct	ctt	cgg	atg	cgt	gag	atg	cgt	aat	ttc	gat	192	
Gln	Val	Ser	Ser	Asn	Pro	Leu	Arg	Met	Arg	Glu	Met	Arg	Asn	Phe	Asp		
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aat	gat	tgc	gta	ggg	agt	gtg	gat	ttt	atc	gag	ttc	atc	aat	gga	cgt	240	
Asn	Asp	Cys	Val	Gly	Ser	Val	Asp	Phe	Ile	Glu	Phe	Ile	Asn	Gly	Arg		
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tcc	agt	ttc	agt	act	gtc	ggg	cag	aag	aat	gct	aaa	ttg	aga	ttt	gca	288	
Ser	Ser	Phe	Ser	Thr	Val	Gly	Gln	Lys	Asn	Ala	Lys	Leu	Arg	Phe	Ala		
				85						90				95			
ccg	att	atc	tat	gat	tgc	gat	aaa	gat	gga	cct	ata	tca	aac	ggg	gag	336	
Pro	Ile	Ile	Tyr	Asp	Cys	Asp	Lys	Asp	Gly	Pro	Ile	Ser	Asn	Gly	Glu		
		100						105						110			
tta	ttt	agg	gtg	ttg	cgt	att	atg	gtt	cat	gac	aat	ctg	agt	gat	aat	384	
Leu	Phe	Arg	Val	Leu	Arg	Ile	Met	Val	His	Asp	Asn	Leu	Ser	Asp	Asn		
		115						120						125			
cag	ctg	cag	cag	cgt	tgc	gat	tgc	acg	cgt	agt	ggc	gga	gat	aat	gac	432	
Gln	Leu	Gln	Gln	Arg	Cys	Asp	Cys	Thr	Arg	Ser	Gly	Gly	Asp	Asn	Asp		

130 135 140  
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 165 170 175  
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 Asp Val  
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 35 40 45  
 Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp  
 50 55 60  
 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg  
 65 70 75 80  
 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala  
 85 90 95  
 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu  
 100 105 110  
 Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn  
 115 120 125  
 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp  
 130 135 140  
 Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg  
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Asp Val

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 Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val  
 15 20 25 30

ggc ttc ggc gac gca atc ttc tac gag tcg ttc gcc ggg gat ttt gat 147  
 Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp  
 35 40 45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tcg gat tcg gcc aag 195  
 Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys  
 50 55 60

aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg 243  
 Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg  
 65 70 75

aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac 291  
 Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp  
 80 85 90

gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339  
 Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp  
 95 100 105 110

tgt gga ggt ccc tgt att aga tat ctt cga acc cag gag agc gga tgg 387  
 Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp  
 115 120 125

aaa ttt gac agc tcc acc atg ttt ggt gct gct aag tat ggc gcg agg 435  
 Lys Phe Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg  
 130 135 140

agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag 483  
 Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu  
 145 150 155

tgt gtt gac cat gat cac aac cag cgg gct tcc ctc aca tcg gac aaa	531
Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys	
160 165 170	
gta cct cgt ttg tac act gga att ctg tcg ccc gaa aat gaa ttc cag	579
Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
175 180 185 190	
atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
195 200 205	
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Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
210 215 220	
ccg tcg aag cgg act gag gac tcg gac gaa aaa gcc aaa atc cca ggc	723
Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
225 230 235	
cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
240 245 250	
atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac	819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
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gca aaa gac cag gca cac gaa cct gag cca aaa cac tgg ggt gct gaa	867
Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
275 280 285	
aag gat ggt gaa tgc gca ccc cca aag att gaa aac gca aag cgg ggg	915
Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
290 295 300	
gcc gcc cct agt tgt ggt gta tcg gag agg caa acc aag att agt cca	963
Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
305 310 315	
aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
320 325 330	
tgg aaa ccc cgc gag atg cta aac cct gga tcg ttc caa atc gca aaa	1059
Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
335 340 345 350	
ccc gct tgt gag cct att gct ggt ata gcc atg gag att agg aag cag	1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
355 360 365	
ggc atc cta tta gac act gtg gtg ggg gtt agg ggg gat aca ggt gaa	1155
Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
370 375 380	

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 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His  
 385 390 395  
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 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro  
 400 405 410  
 tac acc agg tac gta tct aaa atc ccc ggg aaa gcc gat aat ccc ttc 1299  
 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe  
 415 420 425 430  
 tcg agc gag cac aaa tgt aag aat ttc gat ctg att gag gct gag aaa 1347  
 Ser Ser Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys  
 435 440 445  
 cag tgt gcc aat gca gta atc ctg ggt gtt gtg gtt aac tcc ggt tca 1395  
 Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser  
 450 455 460  
 att aac tcc gtt gtg tct tgg ggc tac aaa cct ggc acg gtg aac aag 1443  
 Ile Asn Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys  
 465 470 475  
 aac caa gaa cgc aga gca ccc tcc cag cga cgt agt agc gag att gaa 1491  
 Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu  
 480 485 490  
 gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539  
 Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala  
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 35 40 45  
 Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala  
 50 55 60

Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg Lys Pro  
 65 70 75 80  
 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg  
 85 90 95  
 Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly  
 100 105 110  
 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe  
 115 120 125  
 Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr  
 130 135 140  
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 145 150 155 160  
 Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys Val Pro  
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 Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln Ile Leu  
 180 185 190  
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 195 200 205  
 Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn Pro Ser  
 210 215 220  
 Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly Pro Ser  
 225 230 235 240  
 Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu Ile Leu  
 245 250 255  
 His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His Ala Lys  
 260 265 270  
 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp  
 275 280 285  
 Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly Ala Ala  
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 Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro Asn Tyr  
 305 310 315 320  
 Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile Trp Lys  
 325 330 335  
 Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys Pro Ala  
 340 345 350  
 Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln Gly Ile  
 355 360 365

Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu Glu Tyr  
 370 375 380  
 Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His Ser Leu  
 385 390 395 400  
 Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro Tyr Thr  
 405 410 415  
 Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser  
 420 425 430  
 Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys  
 435 440 445  
 Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn  
 450 455 460  
 Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys Asn Gln  
 465 470 475 480  
 Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu Gly Thr  
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 cgg gtg acc agg gac ggt tcg ggg ccc gga aaa acc ggt gtc aca cgc 99  
 Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg  
 15 20 25  
 ggg tcg tca ccc atg cga tgg gca tgg aag cgg tgg caa gcc gtc ggg 147  
 Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly  
 30 35 40 45  
 gca tcg acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata 195  
 Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile  
 50 55 60

acg aca agc acc cgc gcg cgg cgc tac gcg gtc tcg gcc aaa ttc ccg	243
Thr Thr Ser Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro	
65 70 75	
aga tta agt aat aag ggc aaa gat tac atg cgt tgc gtc ctc caa tac	291
Arg Leu Ser Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr	
80 85 90	
acc gtc aaa aat gaa caa aaa gtt gat tgt ggt ggc tca tat atc aag	339
Thr Val Lys Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys	
95 100 105	
tta tta cct tcg aaa ttg cgc acg ggt gat ggt gat ggc gtg tca gaa	387
Leu Leu Pro Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu	
110 115 120 125	
tat tca att atg ttt ggt cca gat tcg aca ggt gca tca cgt act gtt	435
Tyr Ser Ile Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val	
130 135 140	
cgt cga gct cgc aat tat aag ggt aaa cgg cat ttg cgg aaa aaa gaa	483
Arg Arg Ala Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu	
145 150 155	
cag aat aaa gtg gaa aca gat caa tta aca cat cag tat act acg agt	531
Gln Asn Lys Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser	
160 165 170	
tgg tca cca gat tgg acc tac aac gtt cta gta gat aat aag gaa tcg	579
Trp Ser Pro Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser	
175 180 185	
caa gca ggg aac ctt gcc gac gac tgc gag tta ctt cca cag aag cga	627
Gln Ala Gly Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg	
190 195 200 205	
atc ttc cga ccc agc tgc cga aaa caa tcc aaa cca gtc acc tgc gta	675
Ile Phe Arg Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val	
210 215 220	
gac gtc aag cac cac gcc ccc cga cga aat gtg aaa ccc gcc ggg cac	723
Asp Val Lys His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His	
225 230 235	
gat gac att cca gcg cga cgg acg acg ccg gaa gcg gtc cgg aaa ggc	771
Asp Asp Ile Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly	
240 245 250	
cgc acg aac gag cga ccg gac cgg acg tgg gcg acc ggg acg acc cca	819
Arg Thr Asn Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro	
255 260 265	
cgg cca cgg cgt tac aag gga gag acg aag gcc aaa aag cac cca cgg	867
Arg Pro Arg Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg	
270 275 280 285	



ccg gaa tac aaa ggg acc tgg gtc acg ccg tta cag gac aac ccc act 915  
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cca gcc ccc ccg aac gac cta tat cta ttc ttg gac ctg ggt gca gca 963  
 Pro Ala Pro Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala  
 305 310 315

ggg aca cgg acc tgg acc gtg aaa tcg ggc tca atc acg aac aac atg 1011  
 Gly Thr Arg Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met  
 320 325 330

ata gtg aca acg tcc gtg gaa acc gcg acc gac ttc tca gag aaa acc 1059  
 Ile Val Thr Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr  
 335 340 345

aag gtg gca aac acc acg acc gag ctc aac gac gga cgc gac gcc gga 1107  
 Lys Val Ala Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly  
 350 355 360 365

acg ggg atc ggt gcc gag cgc cac tgt gct gat gag aga tgg aaa gag 1155  
 Thr Gly Ile Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu  
 370 375 380

aca acg gta gcc ccc gat tgc gcc gta tcg gca gcg aac gcc tcg cga 1203  
 Thr Thr Val Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg  
 385 390 395

cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251  
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 35 40 45

Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser  
 50 55 60

Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser  
 65 70 75 80

Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr Thr Val Lys  
 85 90 95  
 Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys Leu Leu Pro  
 100 105 110  
 Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu Tyr Ser Ile  
 115 120 125  
 Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val Arg Arg Ala  
 130 135 140  
 Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu Gln Asn Lys  
 145 150 155 160  
 Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser Trp Ser Pro  
 165 170 175  
 Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser Gln Ala Gly  
 180 185 190  
 Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg Ile Phe Arg  
 195 200 205  
 Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val Asp Val Lys  
 210 215 220  
 His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His Asp Asp Ile  
 225 230 235 240  
 Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly Arg Thr Asn  
 245 250 255  
 Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro Arg Pro Arg  
 260 265 270  
 Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg Pro Glu Tyr  
 275 280 285  
 Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr Pro Ala Pro  
 290 295 300  
 Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala Gly Thr Arg  
 305 310 315 320  
 Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met Ile Val Thr  
 325 330 335  
 Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr Lys Val Ala  
 340 345 350  
 Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly Thr Gly Ile  
 355 360 365  
 Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu Thr Thr Val  
 370 375 380

Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg Arg Thr Gly  
385 390 395 400

Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu Tyr Gly Pro  
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<211> 416

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1 5 10 15

aca aaa gag ctg gga aca gtt atg cgt tca cta gga caa aac cca aca 96  
Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr  
20 25 30

gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac 144  
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn  
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132

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Arg	Asp	Lys	Leu	Arg	Ser	Leu	Cys	Asp	Glu	Lys	Gly	Thr	Pro	Ile	Gln				
690				695					700										
Ser	Leu	Met	Ser	Glu	Leu	Arg	Gly	Met	Glu	Ala	Arg	Leu	Ala	Lys	Ser				
705				710					715				720						
Gly	Asn	Thr	Lys	Ser	Ser	Lys	Glu	Thr	Lys	Ser	Glu	Leu	Ala	Glu	Met				
725				730					735										
Asn	Asn	Gln	Ile	Leu	Tyr	Lys	Ile	Gln	Lys	Glu	Leu	Glu	Val	Arg	Asn				
740				745					750										
Lys	Glu	Leu	His	Val	Ala	Val	Asp	Asn	Ser	Lys	Arg	Leu	Leu	Ser	Glu				
755				760					765										
Asn	Lys	Ile	Leu	Glu	Gln	Asn	Leu	Asn	Ile	Glu	Lys	Lys	Lys	Lys	Glu				
770				775					780										
Glu	Val	Glu	Ile	His	Gln	Lys	Arg	Tyr	Glu	Gln	Glu	Lys	Lys	Val	Leu				
785				790					795				800						
Lys	Leu	Arg	Val	Ser	Glu	Leu	Glu	Asn	Lys	Leu	Glu	Val	Leu	Ala	Gln				
805				810					815										
Asp	Leu	Asp	Ser	Ala	Glu	Ser	Thr	Ile	Glu	Ser	Lys	Asn	Ser	Asp	Met				
820				825					830										
Leu	Leu	Leu	Gln	Asn	Asn	Leu	Lys	Glu	Leu	Glu	Glu	Leu	Arg	Glu	Met				
835				840					845										
Lys	Glu	Asp	Ile	Asp	Arg	Lys	Asn	Glu	Gln	Thr	Ala	Ala	Ile	Leu	Lys				
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Met	Gln	Gly	Ala	Gln	Leu	Ala	Glu	Leu	Glu	Ile	Leu	Tyr	Lys	Glu	Glu				
865				870					875				880						
Gln	Val	Leu	Arg	Lys	Arg	Tyr	Tyr	Asn	Thr	Ile	Glu	Asp	Met	Lys	Gly				
885				890					895										
Lys	Ile	Arg	Val	Tyr	Cys	Arg	Ile	Arg	Pro	Leu	Asn	Glu	Lys	Glu	Ser				
900				905					910										
Ser	Glu	Arg	Glu	Lys	Gln	Met	Leu	Thr	Thr	Val	Asp	Glu	Phe	Thr	Val				
915				920					925										
Glu	His	Ala	Trp	Lys	Asp	Asp	Lys	Arg	Lys	Gln	His	Ile	Tyr	Asp	Arg				
930				935					940										
Val	Phe	Asp	Met	Arg	Ala	Ser	Gln	Asp	Asp	Ile	Phe	Glu	Asp	Thr	Lys				



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 Tyr Leu Val Gln Ser Ala Val Asp Gly Tyr Asn Val Cys Ile Phe Ala  
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 Tyr Gly Gln Thr Gly Ser Gly Lys Thr Phe Thr Ile Tyr Gly His Glu  
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 Ser Asn Pro Gly Leu Thr Pro Arg Ala Thr Lys Glu Leu Phe Asn Ile  
                                  995                      1000                      1005  
 Leu Lys Arg Asp Ser Lys Arg Phe Ser Phe Ser Leu Lys Ala Tyr Met  
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 Val Glu Leu Tyr Gln Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser  
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 Ala Arg Arg Leu Lys Leu Glu Ile Lys Lys Asp Ser Lys Gly Met Val  
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 Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu Glu Leu  
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 Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser Gly Thr  
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 Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser Val Val  
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 Ala Leu Gly Asp Val Ile Gly Ala Leu Ser Ser Gly Asn Gln His Ile  
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 Pro Tyr Arg Asn His Lys Leu Thr Met Leu Met Ser Asp Ser Leu Gly  
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1250

1255

1260

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Lys	Lys	Ala	Arg	Ser	Arg	Leu	Glu	Thr	His	Pro	Arg	Asp	Asn	Glu	Asn	
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Val	Asp	Val	Pro	Val	Ile	Leu	Ser	Thr	Arg	Glu	Ser	Gln	Gly	Thr	Arg	
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Cys	Glu	Trp	Phe	Ala	Thr	Pro	Thr	Asp	Pro	Gln	Arg	Pro	Gly	Val	Tyr	
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Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser	
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Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr	
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cct cca gat cca ctg cag aat cct aat aat tat act agg tat cat aat	624
Pro Pro Asp Pro Leu Gln Asn Pro Asn Asn Tyr Thr Arg Tyr His Asn	
195 200 205	
gat aaa aac agc aag aat agt aac aga aac tac aat aag aga aat aag	672
Asp Lys Asn Ser Lys Asn Ser Asn Arg Asn Tyr Asn Lys Arg Asn Lys	
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Asn Ser Thr Thr Phe Asn Asn Ser Asp Leu Pro Gly His Asn Arg Ser	
225 230 235 240	
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Ser Pro Ala Ile Asn Ala Val Lys Ser Ala Ser Asn Arg Ser Ser Ala	
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ata ggt agt cga aac agt gat tta aac aat gct gct aat gat gaa cgc	816
Ile Gly Ser Arg Asn Ser Asp Leu Asn Asn Ala Ala Asn Asp Glu Arg	
260 265 270	
cat tac gct aga tcg gga aca tat cag ata aac gct gta aca gta ctt	864
His Tyr Ala Arg Ser Gly Thr Tyr Gln Ile Asn Ala Val Thr Val Leu	
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aga gta tta gga aga gga gca cgg cgt gat gta aag tca gca tat cat	912
Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His	
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ggc acc tgt ggt aca ggt ccc cgg atg aaa gtg ata aca ttg gct gtt	960
Gly Thr Cys Gly Thr Gly Pro Arg Met Lys Val Ile Thr Leu Ala Val	
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caa gag aat att aga aac cga att ata ttg gag cta cgg aca tta cac	1008
Gln Glu Asn Ile Arg Asn Arg Ile Ile Leu Glu Leu Arg Thr Leu His	
325 330 335	
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Lys Thr Ser Tyr Gln Tyr Ile Val Pro Tyr Tyr Asp Gly Ile Tyr Thr	
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atc atg aac aaa acg gcg acc ata cgt gcg ccg gtt ttg ggt acg atg	1152
Ile Met Asn Lys Thr Ala Thr Ile Arg Ala Pro Val Leu Gly Thr Met	
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Ala Phe Leu Val Leu Gln Gly Arg Ile Tyr Val His Arg Lys Phe Asp 385 390 395 400	
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agt aat cac gat ata tgg aat aat cgc aat aga gat aaa tat att att Ser Asn His Asp Ile Trp Asn Asn Arg Asn Arg Asp Lys Tyr Ile Ile 530 535 540	1632
agt aac aat cct aat aat agg aat gat aat aat aac act gta tgc gat Ser Asn Asn Pro Asn Asn Arg Asn Asp Asn Asn Asn Thr Val Cys Asp 545 550 555 560	1680
cta agc agt ggc gag tta ggt gaa agt cgt gag gtt gtg cca gac ggt Leu Ser Ser Gly Glu Leu Gly Glu Ser Arg Glu Val Val Pro Asp Gly 565 570 575	1728
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 Thr Ala Asp Leu Gln Arg Trp Gln  
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 Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr  
 35                      40                      45  
 Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser  
 50                      55                      60  
 Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn  
 65                      70                      75                      80  
 Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr  
 85                      90                      95  
 Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg  
 100                      105                      110  
 Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile  
 115                      120                      125  
 Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr  
 130                      135                      140  
 Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn  
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 Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser  
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 Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

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Ser	Pro	Ala	Ile	Asn	Ala	Val	Lys	Ser	Ala	Ser	Asn	Arg	Ser	Ser	Ala
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Ile	Gly	Ser	Arg	Asn	Ser	Asp	Leu	Asn	Asn	Ala	Ala	Asn	Asp	Glu	Arg
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His	Tyr	Ala	Arg	Ser	Gly	Thr	Tyr	Gln	Ile	Asn	Ala	Val	Thr	Val	Leu
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Arg	Val	Leu	Gly	Arg	Gly	Ala	Arg	Arg	Asp	Val	Lys	Ser	Ala	Tyr	His
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Gly	Thr	Cys	Gly	Thr	Gly	Pro	Arg	Met	Lys	Val	Ile	Thr	Leu	Ala	Val
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Gln	Glu	Asn	Ile	Arg	Asn	Arg	Ile	Ile	Leu	Glu	Leu	Arg	Thr	Leu	His
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Lys	Thr	Ser	Tyr	Gln	Tyr	Ile	Val	Pro	Tyr	Tyr	Asp	Gly	Ile	Tyr	Thr
			340					345					350		
Glu	Gly	Ser	Ile	Phe	Ile	Arg	Met	Val	Glu	Leu	Gly	Trp	Val	Thr	Asn
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Ile	Met	Asn	Lys	Thr	Ala	Thr	Ile	Arg	Ala	Pro	Val	Leu	Gly	Thr	Met
				370			375					380			
Ala	Phe	Leu	Val	Leu	Gln	Gly	Arg	Ile	Tyr	Val	His	Arg	Lys	Phe	Asp
				385			390				395				400
Lys	Cys	Pro	Ser	Lys	Arg	Asp	Ile	Lys	Pro	Ser	Asp	Ile	Leu	Val	Asn
				405					410					415	
Asn	Glu	Gly	Arg	Ala	Lys	Ile	Ala	Gly	Phe	Gly	Val	Ser	Gly	Gln	Leu
			420					425						430	
Gln	His	Thr	Leu	Ser	Lys	Asp	Val	Thr	Ser	Val	Glu	Ser	Pro	Glu	Arg
			435				440					445			
Arg	Ser	Gly	Arg	Ser	Tyr	Gly	Phe	Asp	Arg	Asp	Ile	Trp	Ser	Asp	Gly
						455					460				
Ile	Thr	Arg	Val	Ser	Cys	Ala	Ile	Gly	Arg	Phe	Pro	Tyr	Ala	Cys	Asn
						470					475				480
Tyr	Pro	Gln	Gln	Leu	Pro	Gln	Ala	Ser	Gln	His	Gln	Leu	Gln	Gln	Gln

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Ile	Ser	Ala	Val	Asn	Val	Ser	Ala	Gln	Ala	Ser	Leu	Thr	Ala	Asp	Phe	
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Pro	Ala	Leu	Ser	Glu	Thr	Ile	Leu	Lys	Glu	Gly	Arg	Asn	Asn	Gly	Lys	
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Glu	Lys	Ala	Glu	Asn	Ile	Val	Trp	His	Glu	Ser	Ser	Ile	Cys	Arg	Cys	
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Asp	Arg	Gln	Gln	Leu	Gln	Gln	Lys	Gly	Cys	Val	Val	Trp	Ile	Thr		
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Ala	Leu	Phe	Glu	Arg	Gly	Lys	Leu	Thr	Tyr	Thr	Leu	Asp	Gly	Asp	Asn	
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Val	Arg	His	Gly	Leu	Asn	Arg	Asp	Leu	Thr	Phe	Lys	Ala	Glu	His	Arg	
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Thr	Glu	Asn	Ile	Arg	Arg	Ile	Gly	Glu	Val	Ala	Lys	Leu	Phe	Ala	Asp	
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Val	Gly	Val	Ile	Cys	Ile	Ala	Ser	Leu	Ile	Ser	Pro	Tyr	Arg	Arg	Asp	
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Arg	Asp	Ala	Cys	Arg	Ser	Leu	Leu	Pro	Asp	Gly	Asp	Phe	Val	Glu	Val	
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Leu	Tyr	Lys	Leu	Ala	Arg	Ala	Gly	Lys	Ile	Lys	Gly	Phe	Thr	Gly	Ile	
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Asp	Asp	Pro	Tyr	Glu	Ala	Pro	Val	Asn	Cys	Glu	Val	Val	Leu	Lys	His	
		250			255				260					265		
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Thr	Gly	Asp	Asp	Glu	Ser	Cys	Ser	Pro	Arg	Gln	Met	Ala	Glu	Asn	Ile	



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 Leu Lys Glu Gly Arg Asn Asn Gly Lys Glu Lys Ala Glu Asn Ile Val  
 85 90 95  
 Trp His Glu Ser Ser Ile Cys Arg Cys Asp Arg Gln Gln Leu Leu Gln  
 100 105 110  
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 Ser Thr Val Ala Cys Ala Leu Ser Lys Ala Leu Phe Glu Arg Gly Lys  
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 Asp Leu Thr Phe Lys Ala Glu His Arg Thr Glu Asn Ile Arg Arg Ile  
 165 170 175  
 Gly Glu Val Ala Lys Leu Phe Ala Asp Val Gly Val Ile Cys Ile Ala  
 180 185 190  
 Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu  
 195 200 205  
 Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His  
 210 215 220

Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala  
225 230 235 240

Gly Lys Ile Lys Gly Phe Thr Gly Ile Asp Asp Pro Tyr Glu Ala Pro  
245 250 255

Val Asn Cys Glu Val Val Leu Lys His Thr Gly Asp Asp Glu Ser Cys  
260 265 270

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Gly Tyr Leu Glu Gly  
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Ser Gly Ala Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly  
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agc aag gct tcg tct gtg tct gta aga cca agc cct cga act gag ggt 147  
Ser Lys Ala Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly  
30 35 40 45

gag atc tta cag tct cca aat ctc aag agt ttt agc ttt gct gag ctt 195  
Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu  
50 55 60

aaa tca gca acc agg aat ttt aga cca gac agt gtg ctt ggt gaa ggt 243  
Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly  
65 70 75

gga ttc ggt tgt gtt ttc aaa gga tgg att gat gag aag tct ctc act 291  
Gly Phe Gly Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr  
80 85 90

gcc tca aga cca ggc acg ggt ttg gtt att gcc gtc aaa aag ctt aac 339  
Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn  
95 100 105

caa gat ggt tgg caa ggt cac cag gag tgg ctg gct gaa gtg aat tac 387  
Gln Asp Gly Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr

110	115	120	125	
ctt ggt cag ttt tct cac cgt cac ctt gtg aag ctg att ggt tat tgc				435
Leu Gly Gln Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys	130	135	140	
cta gag gat gag cac cgt ctt ctt gtt tac gag ttc atg cct cgg ggt				483
Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly	145	150	155	
agc ttg gag aat cat ctt ttc agg aga ggt ttg tac ttc caa ccg tta				531
Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu	160	165	170	
tct tgg aaa ctt cgg ttg aaa gtt gct ctt ggt gct gca aag gga ctt				579
Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu	175	180	185	
gct ttt ctt cac agt tcc gag aca aga gtg ata tac cga gat ttc aag				627
Ala Phe Leu His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys	190	195	200	205
act tct aat atc ctt ctt gac tcg gag tac aac gca aag ctt tct gat				675
Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp	210	215	220	
ttt ggg ttg gct aag gat ggg cca ata ggt gat aaa agt cat gtc tct				723
Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser	225	230	235	
aca cga gtc atg ggt aca cac gga tat gca gct cct gaa tac ctt gca				771
Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala	240	245	250	
acc ggt cat cta aca aca aag agt gat gtc tat agc ttc ggg gtt gtc				819
Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val	255	260	265	
ctt ctg gag ctg ttg tct ggt cgt cga gca gtg gac aag aac cgc cca				867
Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro	270	275	280	285
tct gga gag agg aac ctt gtg gag tgg gct aaa cca tac ctc gta aac				915
Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn	290	295	300	
aaa aga aag ata ttc cga gtc att gat aat cgt ctt cag gac cag tac				963
Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr	305	310	315	
tct atg gaa gaa gca tgt aaa gtg gct act ctg tct ctg aga tgt ctc				1011
Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu	320	325	330	
acc aca gag att aag ctg aga cca aac atg agc gag gtt gtt tcg cac				1059
Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His	335	340	345	

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Leu Glu His Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp
350 355 360 365

aaa aca gat aga aga atg cgt agg aga agt gac agt gtt gtc agc aaa 1155
Lys Thr Asp Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys
370 375 380

aaa gtg aat gca ggt ttt gct cga cag act gct gtt ggc agt aca gtt 1203
Lys Val Asn Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val
385 390 395

gtt gct tat cct cgc cca tca gcc tcg cca ctg tat gtt tga 1245
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35 40 45

Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu Lys Ser Ala
50 55 60

Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly
65 70 75 80

Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr Ala Ser Arg
85 90 95

Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly
100 105 110

Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln
115 120 125

Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp
130 135 140

Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu
145 150 155 160

Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu Ser Trp Lys

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165                      170                      175  
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 His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys Thr Ser Asn  
                          195                      200                      205  
 Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu  
                          210                      215                      220  
 Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser Thr Arg Val  
                          225                      230                      235                      240  
 Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala Thr Gly His  
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 Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu  
    260                      265                      270  
 Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro Ser Gly Glu  
    275                      280                      285  
 Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn Lys Arg Lys  
    290                      295                      300  
 Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr Ser Met Glu  
    305                      310                      315                      320  
 Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu Thr Thr Glu  
    325                      330                      335  
 Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His Leu Glu His  
    340                      345                      350  
 Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp Lys Thr Asp  
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 Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys Lys Val Asn  
    370                      375                      380  
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 1 5 10

gag caa aat aac ttg cta aag gat ttg gag atg aag gaa act gaa tat 158  
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atg cgc cgt cag agg cat aaa atg gga gct gat gac ttt gag cca ttg 206

Met Arg Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu  
35 40 45

aca atg att ggg aag ggt gca ttc gga gag gtaacatctc ttttatagat 256  
Thr Met Ile Gly Lys Gly Ala Phe Gly Glu  
50 55

catagtctgt tactctgttt tctcagcctc tcattggcat gcacatctt gaaatgttct 316

ctgtgatgca tccttcttga aaggctcttct taggccattt tttttaccac agctaatttt 376

tcaaaaaagt atggcatgct aatttttctc tttctctttg. cag gtt agg atc tgt 431  
Val Arg Ile Cys  
60

agg gag aag gga aca ggc aat gtc tat gca atg aag aag ctt aag aaa 479  
Arg Glu Lys Gly Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys  
65 70 75

tct gag atg ctt cgc aga ggc cag gta tttaaattcc ttcaagtggc 526  
Ser Glu Met Leu Arg Arg Gly Gln Val  
80 85

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Val

gaa cat gta aaa gca gag aga aat tta ctt gca gaa gtt gat agc aat 631  
Glu His Val Lys Ala Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Asn  
90 95 100

tgc att gtc aaa ctg tat tgt tct ttc caa gat gaa gag tac ttg tat 679  
Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln Asp Glu Glu Tyr Leu Tyr  
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ctc ata atg gag tat tta cct ggt ggg gat atg atg act tta ctt atg 727  
Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Met Met Thr Leu Leu Met  
120 125 130

agg aaa gac acc ctg act gaa gac gag gcc agg ttt tat att ggg gaa 775  
Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala Arg Phe Tyr Ile Gly Glu  
135 140 145 150

act gtc ctg gct att gag tcc att cat aag cac aac tac att cac ag 822  
Thr Val Leu Ala Ile Glu Ser Ile His Lys His Asn Tyr Ile His Ar  
155 160 165

gtcagtgaag cagaatatat gatttagttc tagctcccat tggtattttg ttctaaacgt 882

ctttttttct ccaatgtgat acag a gat atc aag cct gat aat ctg cta ctt 934  
g Asp Ile Lys Pro Asp Asn Leu Leu Leu  
s 170 175

gac aaa gac ggc cac atg aaa ttg tca gat ttt gga tta tgt aaa cca 982  
Asp Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro  
180 185 190

tta gac tgt agt aat ctt caa gag aaa gac ttt aca gtt gca aga aac 1030

Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn  
 195 200 205  
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 Val Ser Gly Ala Leu Gln Ser Asp Gly Arg Pro Val Ala Thr Arg Arg  
 210 215 220  
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 Thr Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu  
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 Ala Tyr Ser Thr Val Gly Thr Pro  
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 Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu  
 250 255 260  
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 Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe Pro Asp Glu Val  
 295 300 305  
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 Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg Leu Leu Cys Asn  
 310 315 320  
 gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag 1815  
 Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu Ile Lys  
 325 330 335  
 gtgttgatg cgttgttcaa ctttgagatt caaagttccc ttatgtaaga tcattgtgtg 1875



150

gtaaatcatc tgtttgtatg ctatttgtaa aatcaagatg attacgatcc atgtttgatt 3044

ctctctaacc aaactgtgga aactaaatta acag aa gac gaa aca tct ggt ggg 3098  
lu Asp Glu Thr Ser Gly Gly  
A 445

aca aca acc cac caa gga agc ttt ttg aat cta cta ccg acg cag att 3146  
Thr Thr Thr His Gln Gly Ser Phe Leu Asn Leu Leu Pro Thr Gln Ile  
450 455 460

gaa gat cca gag aaa gaa ggt agt aag tcg agc tca tcc ggg tga 3191  
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20 25 30

Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu Thr Met  
35 40 45

Ile Gly Lys Gly Ala Phe Gly Glu Val Arg Ile Cys Arg Glu Lys Gly  
50 55 60

Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys Ser Glu Met Leu  
65 70 75 80

Arg Arg Gly Gln Val Val Glu His Val Lys Ala Glu Arg Asn Leu Leu  
85 90 95

Ala Glu Val Asp Ser Asn Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln  
100 105 110

Asp Glu Glu Tyr Leu Tyr Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp  
115 120 125

Met Met Thr Leu Leu Met Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala  
130 135 140

Arg Phe Tyr Ile Gly Glu Thr Val Leu Ala Ile Glu Ser Ile His Lys  
145 150 155 160

His Asn Tyr Ile His Arg Asp Ile Lys Pro Asp Asn Leu Leu Leu Asp  
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Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro Leu

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Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
10           15           20           25

cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
           30           35           40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
           45           50           55

agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
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aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
           75           80           85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
           90           95           100           105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
           110           115           120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
           125           130           135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
           140           145           150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
           155           160           165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

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              190              195              200

cat agt aat ccc gta tct aca cgg aca cag tca gaa gag gga agg cta 678
His Ser Asn Pro Val Ser Thr Arg Thr Gln Ser Glu Glu Gly Arg Leu
              205              210              215

tgt gca aaa ggt ggt aaa agc ggt gca cgg cta cta ccc gat cta agt 726
Cys Ala Lys Gly Gly Lys Ser Gly Ala Arg Leu Leu Pro Asp Leu Ser
              220              225              230

act cag gaa caa cta ccc aaa att aat caa gaa aac cct att aat caa 774
Thr Gln Glu Gln Leu Pro Lys Ile Asn Gln Glu Asn Pro Ile Asn Gln
              235              240              245

att gct ttt tca cct agt ccg ttc gtc gtc acg tgc caa acg gaa aga 822
Ile Ala Phe Ser Pro Ser Pro Phe Val Val Thr Cys Gln Thr Glu Arg
250              255              260              265

tcc cta tct caa acg tgg tga ccgtgcaccg gcacggtgaa aaagtcgacc 873
Ser Leu Ser Gln Thr Trp
              270

ggatcgaccg accgaaagcc tgctcgctgg acaaaaaaag agcttttttag gccttttcgct 933
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Gly Arg Tyr Thr Lys Lys Val Ser His Asp Arg Arg Thr Arg Trp Pro
              35              40              45

Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
              50              55              60

Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
              65              70              75              80

Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
              85              90              95

Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
              100              105              110

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Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp  
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 Arg Leu Ile Val Ser Ala Gly Ala Asp Gly Val Ile Ala Val Cys Pro  
 130 135 140  
 Val Ala Gly Glu Cys Asp Asp Asp Ala Arg Asp Gly His Glu Asp  
 145 150 155 160  
 Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu  
 165 170 175  
 Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly  
 180 185 190  
 Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr  
 195 200 205  
 Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser  
 210 215 220  
 Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys  
 225 230 235 240  
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actttccact gtttctttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279
      sp Ser Phe Gly Tyr Thr Thr Asp Glu
      20                      25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327
Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly
      30                      35                      40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375
Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His
      45                      50                      55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423
His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val
      60                      65                      70                      75

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Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu
      80                      85                      90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519
Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
      95                      100                      105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567
Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu
      110                      115                      120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615
Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
      125                      130                      135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660
Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu
      140                      145                      150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720

ggtttgattt ttaaagtttt tggttgacag att agt aaa atc aaa gct aag gta 773
      Ile Ser Lys Ile Lys Ala Lys Val
      155                      160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821
Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val
      165                      170                      175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869
Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu
      180                      185                      190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act 917

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Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr  
 195 200 205 210

gac ctc cgt gac ctt cta ccg aat tcc acc gtt gtc gag gct gga tct 965  
 Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser  
 215 220 225

tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct 1013  
 Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser  
 230 235 240

gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc 1061  
 Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe  
 245 250 255

tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta 1109  
 Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu  
 260 265 270

agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca 1157  
 Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser  
 275 280 285 290

ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta 1203  
 Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr  
 295 300

tcaaattggg gctctgttta gtctcaatgg gaaaacagag aagagggcaa aggtgga 1260

&lt;210&gt; 74

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 74

Met Lys Arg Leu Ser Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr  
 1 5 10 15

Ser Thr Asp Ser Phe Gly Tyr Thr Thr Asp Glu Gln Ser Pro Arg Gly  
 20 25 30

Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala  
 35 40 45

Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser  
 50 55 60

Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys  
 65 70 75 80

Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu  
 85 90 95

Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln  
 100 105 110



Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly  
 115 120 125  
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu  
 130 135 140  
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala  
 145 150 155 160  
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu  
 165 170 175  
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser  
 180 185 190  
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser  
 195 200 205  
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala  
 210 215 220  
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr  
 225 230 235 240  
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly  
 245 250 255  
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp  
 260 265 270  
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro  
 275 280 285  
 Pro Ser Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr  
 290 295 300

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 <213> Arabidopsis thaliana

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 1 5 10  
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 Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu  
 15 20 25  
 ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca 147

Leu Cys Ala Asn Ala Tyr Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala	
30 35 40	
tta cag cag atg aac cgt gcc agt cag tca gtg aat tac cga cga cgt	195
Leu Gln Gln Met Asn Arg Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg	
45 50 55	
gag ctg tca tta atc agc ggc cgg aaa cag ggt gtc cag tct ctg ggt	243
Glu Leu Ser Leu Ile Ser Gly Arg Lys Gln Gly Val Gln Ser Leu Gly	
60 65 70	
tat aga ctt gca cgc ctc gat aac cgc gct ctt gca caa ttg ttg cac	291
Tyr Arg Leu Ala Arg Leu Asp Asn Arg Ala Leu Ala Gln Leu Leu His	
75 80 85 90	
agg gat ggc cag ccc gag gaa gtg gta cag cgc ggc aat gaa atc agc	339
Arg Asp Gly Gln Pro Glu Glu Val Val Gln Arg Gly Asn Glu Ile Ser	
95 100 105	
tat ttc gaa acg gga ctt gaa ccg acc acg ctt aga cgt gtg cgc gat	387
Tyr Phe Glu Thr Gly Leu Glu Pro Thr Thr Leu Arg Arg Val Arg Asp	
110 115 120	
tgt gtt gtt gcc gct ctg cca acc gtt atc tat acc gga ttc aaa cgt	435
Cys Val Val Ala Ala Leu Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg	
125 130 135	
gtt tct cct tac tac gaa ttt atc tcc gtc ggg cgc acg agg gtt gct	483
Val Ser Pro Tyr Tyr Glu Phe Ile Ser Val Gly Arg Thr Arg Val Ala	
140 145 150	
gat cgt ctt agc gaa gtc acg caa gtg gtt ccc cga gat gat aca cgc	531
Asp Arg Leu Ser Glu Val Thr Gln Val Val Pro Arg Asp Asp Thr Arg	
155 160 165 170	
tac gtc tac atc gtg tgg cgg gaa tcc gaa cga tgc aaa tta gag gcg	579
Tyr Val Tyr Ile Val Trp Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala	
175 180 185	
cgg ggg gat ctc cgt gat cgc gat ggt gaa acg ctg gaa aag ttt cgc	627
Arg Gly Asp Leu Arg Asp Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg	
190 195 200	
gtg att gct ttt aac gtc acg ctg gat atc agc agc agt atg gag ccg	675
Val Ile Ala Phe Asn Val Thr Leu Asp Ile Ser Ser Ser Met Glu Pro	
205 210 215	
ctg gcg aag gga gat ttg ccg ccg ttg ctt gct gtt cct gta ggt gaa	723
Leu Ala Lys Gly Asp Leu Pro Pro Leu Leu Ala Val Pro Val Gly Glu	
220 225 230	
caa gct aga ttc agc ttg acg cca acc tgg ttg cca cag ggt cgt agc	771
Gln Ala Arg Phe Ser Leu Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser	
235 240 245 250	
gat gtt tcc agt agt cga cgt ggg cta ccg cgg atg gac aaa gtg cct	819
Asp Val Ser Ser Ser Arg Arg Gly Leu Pro Arg Met Asp Lys Val Pro	

255	260	265	
atc gaa tcc cgt ctc tcg acc gac gga gta ttc agc ttc tcg gta aac			867
Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn			
270	275	280	
gtt aac ggc gct acg cca tcg agg tgg gat cag atg ttg cgc acc gga			915
Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly			
285	290	295	
cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att			963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile			
300	305	310	
ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc			1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr			
315	320	325	330
gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct			1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala			
335	340	345	
cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac			1107
Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr			
350	355	360	
ggg gca gcg cca tga			1122
Gly Ala Ala Pro			
365			

&lt;210&gt; 76

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 76

Met	Asn	Gln	Arg	Ala	Asp	Arg	Asp	Arg	Ala	Ser	Ser	Ile	Arg	Trp	Phe
1				5					10					15	

Ala	Asn	Arg	Leu	Val	Ser	Gly	Ser	Leu	Leu	Leu	Cys	Ala	Asn	Ala	Tyr
	20							25					30		

Ser	Arg	Arg	Thr	Pro	Ala	Ser	Gly	Ala	Ala	Leu	Gln	Gln	Met	Asn	Arg
	35						40					45			

Ala	Ser	Gln	Ser	Val	Asn	Tyr	Arg	Arg	Arg	Glu	Leu	Ser	Leu	Ile	Ser
	50					55					60				

Gly	Arg	Lys	Gln	Gly	Val	Gln	Ser	Leu	Gly	Tyr	Arg	Leu	Ala	Arg	Leu
65				70					75					80	

Asp	Asn	Arg	Ala	Leu	Ala	Gln	Leu	Leu	His	Arg	Asp	Gly	Gln	Pro	Glu
			85						90					95	

Glu	Val	Val	Gln	Arg	Gly	Asn	Glu	Ile	Ser	Tyr	Phe	Glu	Thr	Gly	Leu
			100				105						110		

Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu  
 115 120 125  
 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu  
 130 135 140  
 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val  
 145 150 155 160  
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp  
 165 170 175  
 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp  
 180 185 190  
 Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val  
 195 200 205  
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu  
 210 215 220  
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu  
 225 230 235 240  
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg  
 245 250 255  
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser  
 260 265 270  
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro  
 275 280 285  
 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg  
 290 295 300  
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro  
 305 310 315 320  
 Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys  
 325 330 335  
 Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala Arg Gln Pro Ser Gln Thr  
 340 345 350  
 Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr Gly Ala Ala Pro  
 355 360 365

&lt;210&gt; 77

&lt;211&gt; 1650

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

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 <222> (21)..(203)

<220>  
 <221> CDS  
 <222> (291)..(482)

<220>  
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 <222> (633)..(838)

<220>  
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 <222> (1044)..(1605)

<400> 77

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attcagagaa gaactcacg atg agt atg gat ttt tca cct ttg tta acg gtt 53
      Met Ser Met Asp Phe Ser Pro Leu Leu Thr Val
      1             5             10

ctt gag gga gat ttc aac aag gat aat act tct tct gca aca gaa att 101
Leu Glu Gly Asp Phe Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile
      15             20             25

gat act tta gag aac tta gat gac act agg cag ata agt aaa gga aaa 149
Asp Thr Leu Glu Asn Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys
      30             35             40

cct ccg agg cac ctc aca agc agt gct act agg ctg cag ctt gca gcc 197
Pro Pro Arg His Leu Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala
      45             50             55

aat gcg gtaatat act tgacctgct tttttttttt cttttttttt gttacaatgg 253
Asn Ala
      60

gattcgaatg atgtaactgg tttctgtttg tgcgcag gat gtg gat gtt tgt aac 308
      Asp Val Asp Val Cys Asn
      65

ttg gtt atg aag tca ctt gat gac aaa tca gag ttt cta cct gta tac 356
Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu Pro Val Tyr
      70             75             80

cga tca gga agt tgt gct gag caa ggg gca aaa cag ttc atg gaa gat 404
Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe Met Glu Asp
      85             90             95

gaa cac att tgc atc gat gat ctt gtt aat cat ctt ggt gca gct att 452
Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly Ala Ala Ile
      100            105            110            115

caa tgc tct tct ctt gga gcc ttc tat ggg gtgagtttat cttccaatct 502
Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly
      120            125

tacccaaaga agcataaaag caattcacta gcctgattct tcttttttct ccttttttgt 562

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actagtacga tataagaggt attacttcaa aaactcttct aacatttggt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671  
Val Phe Asp Gly His Gly Thr Asp Ala Ala His Phe  
130 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719  
Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro  
140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767  
Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr  
155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815  
Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala  
175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868  
Leu Thr Ala Phe Ile Phe Gly Ar  
190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt ttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044  
g

agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092  
Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg  
195 200 205 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140  
Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr  
215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188  
Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly  
230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236  
Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His  
245 250 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284  
Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu  
260 265 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332  
Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly  
275 280 285 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380  
Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile  
295 300 305

gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428  
 Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg  
                   310                  315                  320

gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476  
 Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr  
                   325                  330                  335

gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524  
 Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile  
                   340                  345                  350

cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572  
 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn  
                   355                  360                  365                  370

cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625  
 Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro  
                   375                  380

ctttgtgaga ctattgcaa gttag 1650

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                   20                  25                  30

Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu  
                   35                  40                  45

Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp  
                   50                  55                  60

Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu  
                   65                  70                  75                  80

Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe  
                   85                  90                  95

Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly  
                   100                  105                  110

Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp  
                   115                  120                  125

Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu  
                   130                  135                  140

Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala  
 145 150 155 160  
 Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser  
 165 170 175  
 Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe  
 180 185 190  
 Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu  
 195 200 205  
 Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn  
 210 215 220  
 Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr  
 225 230 235 240  
 Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp  
 245 250 255  
 Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu  
 260 265 270  
 Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile  
 275 280 285  
 Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val  
 290 295 300  
 Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys  
 305 310 315 320  
 Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn  
 325 330 335  
 Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile  
 340 345 350  
 Glu Ile Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly  
 355 360 365  
 Leu Asn Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro  
 370 375 380

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 <212> DNA  
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 <400> 79



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              1              5              10

gag gtg cca aag gta gca aca gag gaa tca tcg gca gag gtt aca gat      98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
              15              20              25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca      146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
              30              35              40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca      194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
              45              50              55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac      242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
              60              65              70              75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat      290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
              80              85              90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa      338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
              95              100              105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa      386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
              110              115              120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct      434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
              125              130              135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg      482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
              140              145              150              155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac      530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
              160              165              170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa      575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
              175              180              185

gaagattatc attaa      590

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&lt;210&gt; 80

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 80

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Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp Arg Gly Leu Phe Asp  
 20 25 30

Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile  
 35 40 45

Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu  
 50 55 60

Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser  
 65 70 75 80

Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys  
 85 90 95

Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu  
 100 105 110

Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly  
 115 120 125

His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val  
 130 135 140

Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile  
 145 150 155 160

Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr His Pro Lys Thr Thr  
 165 170 175

Val Glu Glu Glu Lys Lys Asp Lys Glu  
 180 185

<210> 81  
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 1 5 10

gag gtt gcg gcg agg cta gcg gct gag gac ttg cat gac att aac aaa 100  
 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys  
 15 20 25

tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148

Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr	
	30						35					40				
gaa	cat	cca	ccg	gag	caa	gat	agg	ccc	ggt	gtg	ata	ggt	tca	gtg	ttc	196
Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe	
	45					50					55					
agg	gct	gtc	caa	gga	acg	tat	gag	cat	gcg	aga	gac	gct	gta	gtt	gga	244
Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly	
	60				65				70						75	
aaa	acc	cac	gaa	gcg	gct	gag	tct	acc	aaa	gaa	gga	gct	cag	ata	gct	292
Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala	
			80						85					90		
tca	gag	aaa	gcg	gtt	gga	gca	aag	gac	gca	acc	gtc	gag	aaa	gct	aag	340
Ser	Glu	Lys	Ala	Val	Gly	Ala	Lys	Asp	Ala	Thr	Val	Glu	Lys	Ala	Lys	
			95					100					105			
gaa	acc	gct	gat	tat	act	gcg	gag	aag	gtg	ggt	gag	tat	aaa	gac	tat	388
Glu	Thr	Ala	Asp	Tyr	Thr	Ala	Glu	Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	
	110					115						120				
acg	gtt	gat	aaa	gct	aaa	gag	gct	aag	gac	aca	act	gca	gag	aag	gcg	436
Thr	Val	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Thr	Thr	Ala	Glu	Lys	Ala	
	125					130					135					
aag	gag	act	gct	aat	tat	act	gcg	gat	aag	gcg	gtg	gaa	gca	aag	gat	484
Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp	
	140				145					150					155	
aag	acg	gcg	gag	aag	att	ggt	gag	tac	aaa	gac	tat	gcg	gtg	gat	aag	532
Lys	Thr	Ala	Glu	Lys	Ile	Gly	Glu	Tyr	Lys	Asp	Tyr	Ala	Val	Asp	Lys	
			160						165					170		
gca	gta	gaa	gct	aaa	gat	aag	aca	gcg	gag	aag	gcg	aag	gag	act	tcg	580
Ala	Val	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	Lys	Ala	Lys	Glu	Thr	Ser	
			175					180						185		
aat	tat	acg	gcg	gat	aag	gct	aaa	gag	gct	aag	gac	aag	acg	gct	gag	628
Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	
		190					195					200				
aag	gtt	ggt	gag	tat	aag	gat	tac	acg	gtg	gac	aag	gcc	gtg	gaa	gct	676
Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala	
	205					210					215					
agg	gat	tac	aca	gcg	gag	aag	gct	att	gaa	gca	aag	gat	aag	aca	gct	724
Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala	
	220				225					230					235	
gag	aag	act	gga	gag	tat	aag	gac	tat	acg	gtg	gag	aag	gcg	acg	gag	772
Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu	
			240						245					250		
ggg	aaa	gat	gtt	acg	gtg	agt	aag	cta	gga	gag	ctg	aag	gat	agt	gcc	820
Gly	Lys	Asp	Val	Thr	Val	Ser	Lys	Leu	Gly	Glu	Leu	Lys	Asp	Ser	Ala	

255	260	265	
gtt gag aca gcg aag aga gct atg ggt ttc ttg tcg ggg aag aca gag			868
Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu			
270	275	280	
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac			916
Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn			
285	290	295	
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga			964
Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg			
300	305	310	315
ttg gaa ggt aaa gag ctg aaa gaa gaa gct gga gca aaa gcc caa gag			1012
Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu			
320	325	330	
gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc			1060
Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala			
335	340	345	
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg			1108
Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly			
350	355	360	
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa			1156
Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys			
365	370	375	
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag			1204
Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu			
380	385	390	395
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca			1252
His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser			
400	405	410	
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc			1300
Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr			
415	420	425	
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa			1348
Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Ala Arg Lys			
430	435	440	
gat aag gga aag ctg tga gaatactaga			1376
Asp Lys Gly Lys Leu			
445			

&lt;210&gt; 82

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 82

Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala Glu Val Ala Ala Arg  
 1 5 10 15  
 Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys Ser Gly Gly Ala Asp  
 20 25 30  
 Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu  
 35 40 45  
 Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly  
 50 55 60  
 Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala  
 65 70 75 80  
 Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val  
 85 90 95  
 Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr  
 100 105 110  
 Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala  
 115 120 125  
 Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn  
 130 135 140  
 Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys  
 145 150 155 160  
 Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys  
 165 170 175  
 Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp  
 180 185 190  
 Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr  
 195 200 205  
 Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala  
 210 215 220  
 Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu  
 225 230 235 240  
 Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr  
 245 250 255  
 Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys  
 260 265 270  
 Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys  
 275 280 285  
 Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly  
 290 295 300

Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu  
305 310 315 320

Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr  
325 330 335

Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp  
340 345 350

Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala  
355 360 365

Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser  
370 375 380

Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly  
385 390 395 400

Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val  
405 410 415

Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn  
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Asp Val Gly Arg Met Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu  
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<210> 83

<211> 561

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (18) .. (548)

<400> 83

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1 5 10

atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act 98  
Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr  
15 20 25

ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146  
Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln  
30 35 40

gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194  
Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly  
45 50 55

cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242  
Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggt caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

<210> 84  
 <211> 176  
 <212> PRT  
 <213> Arabidopsis thaliana

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 Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro  
 20 25 30  
 Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val  
 35 40 45  
 His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn  
 50 55 60  
 Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg  
 65 70 75 80  
 Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala  
 85 90 95  
 Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met  
 100 105 110

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp  
 115 120 125

Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg  
 130 135 140

Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val  
 145 150 155 160

Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr  
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 <211> 988  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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 <222> (12)..(977)

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tta gtt ttg ttg ttt gct caa gcc aat tcg caa ggt ttg aaa gta ggt 98  
 Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly  
 15 20 25

ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146  
 Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val  
 30 35 40 45

gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194  
 Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu  
 50 55 60

aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242  
 Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val  
 65 70 75

ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290  
 Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn  
 80 85 90

cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338  
 Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu  
 95 100 105

gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386  
 Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu  
 110 115 120 125



gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt 434  
 Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val  
 130 135 140

gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac 482  
 Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn  
 145 150 155

ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc 530  
 Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg  
 160 165 170

tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac 578  
 Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His  
 175 180 185

aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac 626  
 Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn  
 190 195 200 205

ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc 674  
 Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala  
 210 215 220

gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta 722  
 Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu  
 225 230 235

gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg 770  
 Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr  
 240 245 250

cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc 818  
 Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu  
 255 260 265

gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat 866  
 Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His  
 270 275 280 285

ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt 914  
 Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly  
 290 295 300

cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt 962  
 Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys  
 305 310 315

cgg tct gct aat taa gagatataga aa 989  
 Arg Ser Ala Asn  
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<210> 86  
 <211> 321  
 <212> PRT  
 <213> Arabidopsis thaliana

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Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu  
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Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly Phe Tyr Ser  
 20 25 30

Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp  
 35 40 45

Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe  
 50 55 60

Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp  
 65 70 75 80

Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu  
 85 90 95

Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val  
 100 105 110

Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg  
 115 120 125

Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly  
 130 135 140

Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser  
 145 150 155 160

Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly  
 165 170 175

Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly  
 180 185 190

Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly  
 195 200 205

Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu  
 210 215 220

Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp  
 225 230 235 240

Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala  
 245 250 255

Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser  
 260 265 270

Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met  
 275 280 285

Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

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Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala
305          310          315          320

Asn

<210> 87
<211> 650
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (8)...(634)

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          1          5          10

tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc 97
Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro
15          20          25          30

cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct 145
Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala
          35          40          45

tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag 193
Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu
          50          55          60

ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt 241
Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe
          65          70          75

gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct 289
Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala
          80          85          90

aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt 337
Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg
          95          100          105          110

gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt 385
Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val
          115          120          125

aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt 433
Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe
          130          135          140

gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc 481
Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr

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145                      150                      155  
 ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg 529  
 Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser  
 160                      165                      170  
 cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa 577  
 Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu  
 175                      180                      185                      190  
 aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc 625  
 Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser  
 195                      200                      205  
 aag cgt taa gagttttata tatcat 650  
 Lys Arg  
  
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 <212> PRT  
 <213> Arabidopsis thaliana  
  
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 Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu Ser Phe  
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 Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro Arg Ala  
 20                      25                      30  
 Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu  
 35                      40                      45  
 Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val  
 50                      55                      60  
 Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala  
 65                      70                      75                      80  
 Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val  
 85                      90                      95  
 Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala  
 100                      105                      110  
 Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val  
 115                      120                      125  
 Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys  
 130                      135                      140  
 Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly  
 145                      150                      155                      160  
 Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu  
 165                      170                      175

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys  
 180 185 190

Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg  
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<210> 89

<211> 1223

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (16)..(1215)

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gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99  
 Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly  
 15 20 25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147  
 Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro  
 30 35 40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195  
 Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr  
 45 50 55 60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243  
 Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser  
 65 70 75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291  
 Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr  
 80 85 90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339  
 Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp  
 95 100 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387  
 Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser  
 110 115 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435  
 Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser  
 125 130 135 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483  
 Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg  
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caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
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Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
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Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
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Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
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Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
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Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
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Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
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Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
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Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
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Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
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Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr  
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 85 90 95

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Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly  
 115 120 125

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 130 135 140

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 145 150 155 160

Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln  
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Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr  
 180 185 190

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 195 200 205

Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr  
 210 215 220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys  
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 Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val  
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 260 265 270  
 Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly  
 275 280 285  
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 290 295 300  
 Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp  
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 Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala  
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 340 345 350  
 Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys  
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 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu  
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 tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146  
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr  
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aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
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tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
      65                      70                      75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
      80                      85                      90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
      95                      100                      105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
     110                      115                      120                      125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
     130                      135                      140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
     145                      150                      155

gag aag ttt gta caa gat gat tct tct ccg gct tcg gct tga 524
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Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
     35      40      45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
     50      55      60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
     65      70      75      80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

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Arg Leu His	Met Glu Lys Phe Ile Glu Ala Ala Thr Lys Phe Met Glu				
	130		135		140
Trp Lys Lys	Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe Glu Lys Phe				
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Val Gln Asp	Asp Ser Ser Pro Ala Ser Ala				
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 Lys Cys Gly Asp Ser Cys Se  
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tcttataactt ctgttggtttt tttggtatga caaag t tgc gag aag aac tac aac 215  
 r Cys Glu Lys Asn Tyr Asn  
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aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263  
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 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe  
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 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met  
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 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241  
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val  
 65 70 75  
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 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His  
 80 85 90  
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337  
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser  
 95 100 105  
 gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385  
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser  
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 145 150 155

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gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577  
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tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625  
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 225 230 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769  
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aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817  
 Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu  
 255 260 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865  
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&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 96

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 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn  
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 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala  
 145 150 155 160  
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val  
 165 170 175  
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro  
 180 185 190  
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile  
 195 200 205  
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile  
 210 215 220  
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp  
 225 230 235 240  
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val  
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ctt gga agc gcc cgt gtg aca atg agg aag act gtt gcc aag cca aag	146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys	
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Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu	
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ggt cca ttc tct gcc gaa tca ccg agc tac ctt acc gga gag ttc ccc	242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro	
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gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca	290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr	
80 85 90	
ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg	338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met	
95 100 105	
ctc gga gcc cta gcc tgc gtc ttc cct gag ctt ttg gct aga aac gga	386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly	
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Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe	
125 130 135	
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Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala	
140 145 150 155	
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Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala	
160 165 170	
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Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu	
175 180 185	
gac ttg ctt tac ccc ggt gcc agc ttc gac cca ttg ggt ttg gct acc	626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr	
190 195 200	
gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga	674

Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly  
 205 210 215  
 aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722  
 Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val  
 220 225 230 235  
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 Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro  
 240 245 250  
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 Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp  
 65 70 75 80  
 Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg  
 85 90 95  
 Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
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 Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu  
 115 120 125  
 Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu  
 130 135 140  
 Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala  
 145 150 155 160  
 Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg  
 165 170 175

Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro  
 180 185 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe  
 195 200 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe  
 210 215 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro  
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ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146  
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu  
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cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194  
 Pro Phe Ile Leu Arg Asn  
 45 50

atattgtatt tcatttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254



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 85 90 95  
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 115 120 125  
 act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt 654  
 Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val  
 130 135 140 145  
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 Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe  
 150 155 160  
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 Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly  
 165 170 175  
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 Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp  
 180 185 190  
 gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa 843  
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&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

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      50                      55                      60
Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser
      65                      70                      75                      80
Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile
                        85                      90                      95
Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser
                        100                    105                    110
Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr
                        115                    120                    125
Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu
      130                    135                    140
Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp
      145                    150                    155                    160
His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu
                        165                    170                    175
Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser
                        180                    185                    190
Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
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 Thr Ala Gly Lys Ala Gl  
 15

cttaaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157  
 actagaaatt tcagttactt gtttaattta gtttgcgta attatgtaat tgatgatttt 217

atggttacaa tgggtgtcat gta g gag aag agc aat gtt ctg ctg gac aag 268  
 u Glu Lys Ser Asn Val Leu Leu Asp Lys  
 20 25

gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319  
 Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gln Gl  
 30 35 40

ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379  
 gtacgcagat ttctgatatg gttatgtata tgttata g gcg gga aag agt gta 432  
 n Ala Gly Lys Ser Val  
 45

tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480  
 Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly  
 50 55 60

ctg aac aag tag agattcgggt caaatttggg 512  
 Leu Asn Lys  
 65

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Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala  
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 35 40 45

Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu  
 50 55 60

Asn Lys  
 65

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gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac 97  
 Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp  
 15 20 25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt 145  
 Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val  
 30 35 40 45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag 193  
 Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys  
 50 55 60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt 241  
 Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu  
 65 70 75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct 289  
 Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala  
 80 85 90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt 337  
 Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val  
 95 100 105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag 385  
 Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys  
 110 115 120 125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag 433  
 Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln  
 130 135 140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga 481  
 Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg  
 145 150 155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag 529  
 Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys  
 160 165 170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc 577  
 Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe  
 175 180 185

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atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625
Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
190 195 200 205

ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673
Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly
210 215 220

tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721
Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr
225 230 235

gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769
Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln
240 245 250

aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817
Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr
255 260 265

att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865
Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr
270 275 280 285

ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913
Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val
290 295 300

ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca 961
Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro
305 310 315

tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt 1009
Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val
320 325 330

cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057
Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg
335 340 345

gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105
Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr
350 355 360 365

tta aac act gag ctc tga gctcaagtct tgttt 1138
Leu Asn Thr Glu Leu
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&lt;210&gt; 104

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 104

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Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser	35	40	45
Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His	50	55	60
Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu	65	70	75
Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp	85	90	95
Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val	100	105	110
Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln	115	120	125
Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg	130	135	140
Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys	145	150	155
Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp	165	170	175
Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu	180	185	190
Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys	195	200	205
Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe	210	215	220
Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu	225	230	235
Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu	245	250	255
Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser	260	265	270
Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala	275	280	285
His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro	290	295	300
Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro Tyr Met Ala			

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		Met	Ala	Gly	Lys	Gly	Gly	Lys	Gly	Leu	Val	Ala						
		1				5					10							
gcg aag acg atg gct gct aac aag gac aaa gac aag gac aag aag aaa		100																
Ala Lys Thr Met Ala Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys																		
	15					20						25						
ccc atc tct cgc tct gct cgt gct ggt att cag ttt cca gtt gga cga		148																
Pro Ile Ser Arg Ser Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg																		
	30					35					40							
att cac agg caa ctg aag acc cga gtc tcg gca cat ggc aga gtt ggt		196																
Ile His Arg Gln Leu Lys Thr Arg Val Ser Ala His Gly Arg Val Gly																		
	45					50				55								
gcc act gca gcc gtc tac aca gct tca atc ctg gag tat ctg aca gca		244																
Ala Thr Ala Ala Val Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala																		
	60				65				70			75						
gag gtt ctt gag ttg gct ggg aat gcg agc aag gat ctc aaa gtg aag		292																
Glu Val Leu Glu Leu Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys																		
	80							85				90						
agg ata acg cca agg cat ctg cag ttg gcg att aga gga gat gag gag		340																
Arg Ile Thr Pro Arg His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu																		
	95						100					105						
ctg gac aca ctc atc aag gga acg att gct gga ggt ggt gtg atc cct		388																
Leu Asp Thr Leu Ile Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro																		
	110					115						120						

cac atc cac aag tct ctc atc aac aaa acc acc aag gag tga 430  
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<212> PRT

<213> Arabidopsis thaliana

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Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu  
 35 40 45

Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val  
 50 55 60

Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu  
 65 70 75 80

Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg  
 85 90 95

His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile  
 100 105 110

Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser  
 115 120 125

Leu Ile Asn Lys Thr Thr Lys Glu  
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tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt	97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
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gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
110 115 120	
aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
145 150 155	
tgg gat ttt agt tac acc tat tta ctg cca tgt cct tat atc tcg gat	529
Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769

Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg  
 240 245 250  
 ctt cgt ttt aat gtc aag cgt tgt gta tca tat tcg ctt gat gaa gag 817  
 Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu  
 255 260 265  
 agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct 865  
 Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Asp Leu Cys Pro  
 270 275 280  
 att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg 913  
 Ile Glu Asn Leu Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met  
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 Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg Lys Thr Ile Ser  
 35 40 45  
 Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val  
 50 55 60  
 Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro  
 65 70 75 80  
 Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg  
 85 90 95  
 Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr  
 100 105 110  
 Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His  
 115 120 125  
 Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln  
 130 135 140  
 Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser  
 145 150 155 160  
 Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr  
 165 170 175

Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly  
 180 185 190  
 Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His  
 195 200 205  
 Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp  
 210 215 220  
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn  
 225 230 235 240  
 Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn  
 245 250 255  
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro  
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gataccta	aaa	ccaaatccaa	ttca	atg	gcg	gaa	gaa	gca	aaa	tcc	aaa	gga	171			
				Met	Ala	Glu	Glu	Ala	Lys	Ser	Lys	Gly				
				1				5								
aac	gca	gct	tct	tcc	ggc	gat	tac	gcc	acc	gca	ata	acc	cat	ttc	219	
Asn	Ala	Ala	Phe	Ser	Ser	Gly	Asp	Tyr	Ala	Thr	Ala	Ile	Thr	His	Phe	
10					15				20					25		
aca	gaa	gca	atc	aac	ctt	tca	cca	acc	aat	cac	atc	ctc	tac	tca	aac	267
Thr	Glu	Ala	Ile	Asn	Leu	Ser	Pro	Thr	Asn	His	Ile	Leu	Tyr	Ser	Asn	
				30					35					40		
aga	tcc	gct	tct	tac	gct	tct	ctc	cac	cgt	tac	gaa	gaa	gct	tta	tca	315
Arg	Ser	Ala	Ser	Tyr	Ala	Ser	Leu	His	Arg	Tyr	Glu	Glu	Ala	Leu	Ser	
			45					50					55			
gac	gcg	aag	aag	act	ata	gag	ctt	aaa	cct	gat	tgg	tct	aaa	gga	tat	363
Asp	Ala	Lys	Lys	Thr	Ile	Glu	Leu	Lys	Pro	Asp	Trp	Ser	Lys	Gly	Tyr	
		60					65					70				
agc	cga	tta	ggt	gct	gcg	ttt	att	gga	ttg	tcc	aag	ttt	gat	gaa	gcg	411
Ser	Arg	Leu	Gly	Ala	Ala	Phe	Ile	Gly	Leu	Ser	Lys	Phe	Asp	Glu	Ala	
	75					80					85					
gtt	gat	tcg	tat	aag	aaa	gga	tta	gag	att	gat	ccg	agt	aat	gag	atg	459
Val	Asp	Ser	Tyr	Lys	Lys	Gly	Leu	Glu	Ile	Asp	Pro	Ser	Asn	Glu	Met	
90					95					100				105		
ctt	aaa	tcg	gga	tta	gct	gat	gct	tcg	aga	tct	agg	gtt	tcg	tca	aag	507
Leu	Lys	Ser	Gly	Leu	Ala	Asp	Ala	Ser	Arg	Ser	Arg	Val	Ser	Ser	Lys	
			110						115					120		
tcg	aat	cct	ttt	gtt	gat	gcg	ttt	caa	ggg	aag	gag	atg	tgg	gag	aag	555
Ser	Asn	Pro	Phe	Val	Asp	Ala	Phe	Gln	Gly	Lys	Glu	Met	Trp	Glu	Lys	
			125				130						135			
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Leu	Thr	Ala	Asp	Pro	Gly	Thr	Arg	Val	Tyr	Leu	Glu	Gln	Asp	Asp	Phe	
		140				145						150				
gtt	aag	acg	atg	aag	gag	att	cag	agg	aac	cct	aat	aat	ctt	aat	ttg	651
Val	Lys	Thr	Met	Lys	Glu	Ile	Gln	Arg	Asn	Pro	Asn	Asn	Leu	Asn	Leu	
	155					160					165					
tat	atg	aag	gat	aag	aga	gtt	atg	aag	gct	tta	ggg	gtt	ttg	ttg	aat	699
Tyr	Met	Lys	Asp	Lys	Arg	Val	Met	Lys	Ala	Leu	Gly	Val	Leu	Leu	Asn	
170					175					180				185		
gtg	aag	ttt	ggt	gga	tct	agt	ggt	gaa	gat	act	gag	atg	aag	gag	gct	747
Val	Lys	Phe	Gly	Gly	Ser	Ser	Gly	Glu	Asp	Thr	Glu	Met	Lys	Glu	Ala	
			190						195					200		
gat	gag	agg	aaa	gag	cct	gaa	ccg	gag	atg	gaa	cct	atg	gag	ttg	acg	795
Asp	Glu	Arg	Lys	Glu	Pro	Glu	Pro	Glu	Met	Glu	Pro	Met	Glu	Leu	Thr	
			205					210					215			
gag	gag	gag	agg	cag	aag	aag	gag	aga	aag	gag	aag	gct	ttg	aag	gag	843

Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys Glu  
 220 225 230  
 aaa ggg gaa gga aat gtt gct tat aag aag aag gat ttt ggg aga gct 891  
 Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Gly Arg Ala  
 235 240 245  
 gtt gaa cat tat act aag gcc atg gag ctc gat gat gag gat att tcg 939  
 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser  
 250 255 260 265  
 tat ttg acg aat cgt gct gct gtt tat ctt gag atg ggg aag 981  
 Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys  
 270 275  
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 ttgtgatgac cttgatgggt ttgataact ttcacatgct tcttggttga gatttaagag 1161  
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 gtgatgtttt acttcatttc tcaaataaaa ttatcag tac gag gag tgc att gaa 1456  
 Tyr Glu Glu Cys Ile Glu  
 280 285  
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 Asp Cys Asp Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe  
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 Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp  
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 cct acg ata gcc gag gag gag cga gag aaa g gtatatatac tgatcctcag 1747  
 Pro Thr Ile Ala Glu Glu Glu Arg Glu Lys G  
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 ly Asn Gly Phe Phe Lys Glu Gln Lys Tyr Pro Glu Ala Val  
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 Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu Lys His Asp Pro Lys  
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 Val  
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Val Gln Val Arg  
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35 40 45

Leu His Arg Tyr Glu Glu Ala Leu Ser Asp Ala Lys Lys Thr Ile Glu  
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Leu Lys Pro Asp Trp Ser Lys Gly Tyr Ser Arg Leu Gly Ala Ala Phe  
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Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly  
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Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp  
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Ala Ser Arg Ser Arg Val Ser Ser Lys Ser Asn Pro Phe Val Asp Ala  
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Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr  
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Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile  
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Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val  
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Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser  
180 185 190

Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu  
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Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys  
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Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

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 Val Tyr Leu Glu Met Gly Lys Tyr Glu Glu Cys Ile Glu Asp Cys Asp  
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 Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe Lys Met Ile  
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 Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys Met Ala Arg  
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 Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu  
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 Asp Pro Ser Phe Thr Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe  
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535

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&lt;220&gt;

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&lt;222&gt; (622)..(1480)

&lt;400&gt; 111

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ataagagaga gagaagaaaa aaagaattac aattaataag aacaagatca agaatcaaga 120

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Gly Pro Trp Ser Pro Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu

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25

30

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Asn Ser Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile G

35

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actttgagac cgtgggtcgtg tttaaatttgt gtgttgatga tatttattta catggtatag 385

gt tta agg aga tgt ggg aag agt tgc agg cta agg tgg ctc aac tat 432

ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr

50

55

60

ttg aga cca aac atc aaa cat ggt ggc ttc tcc gag gaa gaa gac aac 480

Leu Arg Pro Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn

65

70

75

atc att tgt aac ctc tat gtt act att ggt agc ag gtactatata 525

Ile Ile Cys Asn Leu Tyr Val Thr Ile Gly Ser Ar

80

85

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g Trp Ser Ile Ile Ala Ala  
90 95

caa tgg ttt ggg agc agt aac ttt cag aca gaa gca atc aac gat atg 1264  
Gln Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met  
290 295 300

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 Thr Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala  
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 Ala Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile  
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 Ser Trp Glu Asp Ile Thr Ser Leu Val Asn Ser Glu Asp Ala Ser Tyr  
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 Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro  
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 Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn Ile Ile Cys  
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 Asn Leu Tyr Val Thr Ile Gly Ser Arg Trp Ser Ile Ile Ala Ala Gln  
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 Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Arg  
 100 105 110  
 Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu Ala  
 115 120 125  
 Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly Gln  
 130 135 140

Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn Met  
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 His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr Tyr  
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 Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr Leu  
 195 200 205  
 Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro Asp  
 210 215 220  
 His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe Ser  
 225 230 235 240  
 Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly Gly  
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 Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu Pro  
 260 265 270  
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 Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala Ala  
 325 330 335  
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Gly	Ser	Ser	Val	Ala	Lys	Leu	Ala	Ile	Arg	Arg	Thr	Leu	Ser	Gln	Ser		
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Arg	Cys	Gly	Ser	Tyr	Ala	Thr	Arg	Thr	Arg	Val	Leu	Pro	Cys	Gln	Thr		
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Arg	Cys	Phe	His	Ser	Thr	Ile	Leu	Lys	Ser	Lys	Ala	Glu	Ser	Ala	Ala		
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cct	ggt	cca	cgt	cct	gtc	cca	ctt	tct	aag	cta	act	gat	agc	ttc	tta		247
Pro	Val	Pro	Arg	Pro	Val	Pro	Leu	Ser	Lys	Leu	Thr	Asp	Ser	Phe	Leu		
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Asp	Gly	Thr	Ser	Ser	Val	Tyr	Leu	Glu	Glu	Leu	Gln	Arg	Ala	Trp	Glu		
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gct	gat	ccc	aac	agt	ggt	gat	gag	tcg	tgg	gat	aac	ttt	ttt	agg	aat		343
Ala	Asp	Pro	Asn	Ser	Val	Asp	Glu	Ser	Trp	Asp	Asn	Phe	Phe	Arg	Asn		
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Phe	Val	Gly	Gln	Ala	Ser	Thr	Ser	Pro	Gly	Ile	Ser	Gly	Gln	Thr	Ile		
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caa	gaa	agc	atg	cgt	ttg	ttg	ttg	cta	ggt	aga	gct	tac	cag	ggt	aat		439

Gln	Glu	Ser	Met	Arg	Leu	Leu	Leu	Leu	Val	Arg	Ala	Tyr	Gln	Val	Asn		
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Gly	His	Met	Lys	Ala	Lys	Leu	Asp	Pro	Leu	Gly	Leu	Glu	Lys	Arg	Glu		
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Ile	Pro	Glu	Asp	Leu	Thr	Pro	Gly	Leu	Tyr	Gly	Phe	Thr	Glu	Ala	Asp		
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Leu	Asp	Arg	Glu	Phe	Phe	Leu	Gly	Val	Trp	Arg	Met	Ser	Gly	Phe	Leu		
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tct	gag	aac	cgc	ccg	gtt	caa	aca	ctg	agg	tcg	ata	ctg	tcg	agg	ctt	631	
Ser	Glu	Asn	Arg	Pro	Val	Gln	Thr	Leu	Arg	Ser	Ile	Leu	Ser	Arg	Leu		
		185					190					195					
gag	caa	gct	tac	tgt	ggg	act	ata	ggg	tat	gag	tac	atg	cac	att	gct	679	
Glu	Gln	Ala	Tyr	Cys	Gly	Thr	Ile	Gly	Tyr	Glu	Tyr	Met	His	Ile	Ala		
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Asp	Arg	Asp	Lys	Cys	Asn	Trp	Leu	Arg	Asp	Lys	Ile	Glu	Thr	Pro	Thr		
215					220					225					230		
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Pro	Arg	Gln	Tyr	Asn	Ser	Glu	Arg	Arg	Met	Val	Ile	Tyr	Asp	Arg	Leu		
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Thr	Trp	Ser	Thr	Gln	Phe	Glu	Asn	Phe	Leu	Ala	Thr	Lys	Trp	Thr	Thr		
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Lys	Glu	Met	Phe	Asp	Arg	Ser	Ala	Asp	Leu	Gly	Val	Glu	Asn	Ile	Val		
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Ile	Gly	Met	Pro	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Gly	Asn	Val	Val		
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aga	aaa	cct	cta	cgc	caa	ata	ttc	agc	gag	ttt	agc	ggt	ggt	act	agg	1015	
Arg	Lys	Pro	Leu	Arg	Gln	Ile	Phe	Ser	Glu	Phe	Ser	Gly	Gly	Thr	Arg		
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Pro	Val	Asp	Glu	Val	Gly	Leu	Tyr	Thr	Gly	Thr	Gly	Asp	Val	Lys	Tyr		
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His Leu Ser Leu Val Ala Asn Pro Ser	His Leu Glu Ala Val Asp Pro		
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Val Val Ile Gly Lys Thr Arg Ala Lys Gln Tyr	Tyr Thr Lys Asp Glu		
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Asn Arg Thr Lys Asn Met Gly Ile Leu Ile His	Gly Asp Gly Ser Phe		
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Ala Gly Gln Gly Val Val Tyr Glu Thr Leu His	Leu Ser Ala Leu Pro		
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Asn Tyr Cys Thr Gly Gly Thr Val His Ile Val	Val Asn Asn Gln Val		
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Asp Val Ala Lys Ala Leu Ser Ala Pro Ile Phe	His Val Asn Ala Asp		
455	460	465	
gac att gaa gca gta gtg cat gct tgt gag ctt	gct gct gag tgg cgc	1495	
Asp Ile Glu Ala Val Val His Ala Cys Glu Leu	Ala Ala Glu Trp Arg		
475	480	485	
cag acg ttc cat tct gat gtt gtt gtt gat tta	gta tgc tac cgt cgc	1543	
Gln Thr Phe His Ser Asp Val Val Val Asp	Leu Val Cys Tyr Arg Arg		
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Phe Gly His Asn Glu Ile Asp Glu Pro Ser Phe	Thr Gln Pro Lys Met		
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Tyr Lys			
520			
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Val Ile Arg Ser His Pro Ser Ser Leu Gln	Ile Tyr Gln Glu		
525	530		
aag ctc ttg caa tct gga cag gta acc caa gaa	gat att gat aag att	1806	
Lys Leu Leu Gln Ser Gly Gln Val Thr Gln	Glu Asp Ile Asp Lys Ile		
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 Pro His Arg Gly Val Lys Arg Val Tyr Glu Gln Arg Ala Gln Met Ile  
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 Glu Ser Gly Glu Gly Ile Asp Trp Gly Leu Gly Glu Ala Leu Ala Phe  
 635 640 645  
 gct aca ctg gtt gtg gaa ggg aac cat gtt cgg cta agt ggt caa gat 2259  
 Ala Thr Leu Val Val Glu Gly Asn His Val Arg Leu Ser Gly Gln Asp  
 650 655 660 665  
 gtt gaa aga gga act ttc agt cat aga cac tca gtg ctt cat gat caa 2307  
 Val Glu Arg Gly Thr Phe Ser His Arg His Ser Val Leu His Asp Gln  
 670 675 680  
 gaa acc ggg gag gaa tat tgt ccc ctc gat cac cta atc aaa aac caa 2355  
 Glu Thr Gly Glu Glu Tyr Cys Pro Leu Asp His Leu Ile Lys Asn Gln  
 685 690 695  
 gac cct gaa atg ttc act gtc agc aac ag gtagcatgtt ttttttaatc 2404  
 Asp Pro Glu Met Phe Thr Val Ser Asn Se  
 700 705  
 tctagagatg ataaccactc ttcaattggt tttacatgat ctttacgttg tttgtgtatg 2464  
 cag c tcc ctt tca gaa ttt ggt gtt ctc ggt ttc gaa ctg ggt tat tcg 2513  
 r Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu Gly Tyr Se  
 710 715 720  
 atg gaa aat ccc aat tct ctg gtg ata tgg gaa gct cag ttt gga gac 2561  
 r Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln Phe Gly As  
 725 730 735  
 ttt gct aat ggc gca caa gtt atg ttt gat cag ttc ata agc agt ggg 2609  
 p Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile Ser Ser Gl



214

acc ccc gtc atc cct taa aaaaacacag cttgaga 3790  
Thr Pro Val Ile Pro  
970

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              20              25              30

Val Leu Pro Cys Gln Thr Arg Cys Phe His Ser Thr Ile Leu Lys Ser
      35              40              45

Lys Ala Glu Ser Ala Ala Pro Val Pro Arg Pro Val Pro Leu Ser Lys
      50              55              60

Leu Thr Asp Ser Phe Leu Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu
  65              70              75              80

Leu Gln Arg Ala Trp Glu Ala Asp Pro Asn Ser Val Asp Glu Ser Trp
              85              90              95

Asp Asn Phe Phe Arg Asn Phe Val Gly Gln Ala Ser Thr Ser Pro Gly
      100              105              110

Ile Ser Gly Gln Thr Ile Gln Glu Ser Met Arg Leu Leu Leu Leu Val
      115              120              125

Arg Ala Tyr Gln Val Asn Gly His Met Lys Ala Lys Leu Asp Pro Leu
  130              135              140

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Gly Leu Glu Lys Arg Glu Ile Pro Glu Asp Leu Thr Pro Gly Leu Tyr  
 145 150 155 160  
 Gly Phe Thr Glu Ala Asp Leu Asp Arg Glu Phe Phe Leu Gly Val Trp  
 165 170 175  
 Arg Met Ser Gly Phe Leu Ser Glu Asn Arg Pro Val Gln Thr Leu Arg  
 180 185 190  
 Ser Ile Leu Ser Arg Leu Glu Gln Ala Tyr Cys Gly Thr Ile Gly Tyr  
 195 200 205  
 Glu Tyr Met His Ile Ala Asp Arg Asp Lys Cys Asn Trp Leu Arg Asp  
 210 215 220  
 Lys Ile Glu Thr Pro Thr Pro Arg Gln Tyr Asn Ser Glu Arg Arg Met  
 225 230 235 240  
 Val Ile Tyr Asp Arg Leu Thr Trp Ser Thr Gln Phe Glu Asn Phe Leu  
 245 250 255  
 Ala Thr Lys Trp Thr Thr Ala Lys Arg Phe Gly Leu Glu Gly Ala Glu  
 260 265 270  
 Ser Leu Ile Pro Gly Met Lys Glu Met Phe Asp Arg Ser Ala Asp Leu  
 275 280 285  
 Gly Val Glu Asn Ile Val Ile Gly Met Pro His Arg Gly Arg Leu Asn  
 290 295 300  
 Val Leu Gly Asn Val Val Arg Lys Pro Leu Arg Gln Ile Phe Ser Glu  
 305 310 315 320  
 Phe Ser Gly Gly Thr Arg Pro Val Asp Glu Val Gly Leu Tyr Thr Gly  
 325 330 335  
 Thr Gly Asp Val Lys Tyr His Leu Gly Thr Ser Tyr Asp Arg Pro Thr  
 340 345 350  
 Arg Gly Gly Lys His Leu His Leu Ser Leu Val Ala Asn Pro Ser His  
 355 360 365  
 Leu Glu Ala Val Asp Pro Val Val Ile Gly Lys Thr Arg Ala Lys Gln  
 370 375 380  
 Tyr Tyr Thr Lys Asp Glu Asn Arg Thr Lys Asn Met Gly Ile Leu Ile  
 385 390 395 400  
 His Gly Asp Gly Ser Phe Ala Gly Gln Gly Val Val Tyr Glu Thr Leu  
 405 410 415  
 His Leu Ser Ala Leu Pro Asn Tyr Cys Thr Gly Gly Thr Val His Ile  
 420 425 430  
 Val Val Asn Asn Gln Val Ala Phe Thr Thr Asp Pro Arg Glu Gly Arg  
 435 440 445

Ser Ser Gln Tyr Cys Thr Asp Val Ala Lys Ala Leu Ser Ala Pro Ile  
 450 455 460  
 Phe His Val Asn Ala Asp Asp Ile Glu Ala Val Val His Ala Cys Glu  
 465 470 475 480  
 Leu Ala Ala Glu Trp Arg Gln Thr Phe His Ser Asp Val Val Val Asp  
 485 490 495  
 Leu Val Cys Tyr Arg Arg Phe Gly His Asn Glu Ile Asp Glu Pro Ser  
 500 505 510  
 Phe Thr Gln Pro Lys Met Tyr Lys Val Ile Arg Ser His Pro Ser Ser  
 515 520 525  
 Leu Gln Ile Tyr Gln Glu Lys Leu Leu Gln Ser Gly Gln Val Thr Gln  
 530 535 540  
 Glu Asp Ile Asp Lys Ile Gln Lys Lys Val Ser Ser Ile Leu Asn Glu  
 545 550 555 560  
 Glu Tyr Glu Ala Ser Lys Asp Tyr Ile Pro Gln Lys Arg Asp Trp Leu  
 565 570 575  
 Ala Ser His Trp Thr Gly Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile  
 580 585 590  
 Arg Asn Thr Gly Val Lys Pro Glu Ile Leu Lys Asn Val Gly Lys Ala  
 595 600 605  
 Ile Ser Thr Phe Pro Glu Asn Phe Lys Pro His Arg Gly Val Lys Arg  
 610 615 620  
 Val Tyr Glu Gln Arg Ala Gln Met Ile Glu Ser Gly Glu Gly Ile Asp  
 625 630 635 640  
 Trp Gly Leu Gly Glu Ala Leu Ala Phe Ala Thr Leu Val Val Glu Gly  
 645 650 655  
 Asn His Val Arg Leu Ser Gly Gln Asp Val Glu Arg Gly Thr Phe Ser  
 660 665 670  
 His Arg His Ser Val Leu His Asp Gln Glu Thr Gly Glu Glu Tyr Cys  
 675 680 685  
 Pro Leu Asp His Leu Ile Lys Asn Gln Asp Pro Glu Met Phe Thr Val  
 690 695 700  
 Ser Asn Ser Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu  
 705 710 715 720  
 Gly Tyr Ser Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln  
 725 730 735  
 Phe Gly Ap Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile  
 740 745 750

Ser Ser Gy Glu Ala Lys Trp Leu Arg Gln Thr Gly Leu Val Val Leu  
 755 760 765  
 Leu Pro Hs Gly Tyr Asp Gly Gln Gly Pro Glu His Ser Ser Gly Arg  
 770 775 780  
 Leu Glu Ag Phe Leu Gln Met Ser Asp Asp Asn Pro Tyr Val Ile Pro  
 785 790 795  
 Glu Met Asp Pro Thr Leu Arg Lys Gln Ile Gln Glu Cys Asn Trp Gln  
 800 805 810  
 Val Val Asn Val Thr Thr Pro Ala Asn Trp Phe His Val Leu Arg Arg  
 815 820 825  
 Gln Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys  
 830 835 840  
 Asn Leu Leu Arg His Lys Gln Cys Val Ser Asn Leu Ser Glu Phe Asp  
 845 850 855  
 Asp Val Lys Gly His Pro Gly Phe Asp Lys Gln Gly Thr Arg Phe Lys  
 860 865 870  
 Arg Leu Ile Lys Asp Gln Ser Gly His Ser Asp Leu Glu Glu  
 875 880 885  
 Asp Ala Glu Ile Val Trp Cys Gln Glu Glu Pro Met Asn Met Gly Gly  
 890 895 900  
 Tyr Gln Tyr Ile Ala Leu Arg Leu Cys Thr Ala Met Lys Ala Leu Gln  
 905 910 915  
 Arg Gly Asn Phe Asn Asp Ile Lys Tyr Val Gly Arg Leu Pro Ser Ala  
 920 925 930  
 Ala Thr Ala Thr Gly Phe Tyr Gln Leu His Val Lys Glu Gln Thr Asp  
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&lt;221&gt; CDS

&lt;222&gt; (465)..(662)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (783)..(1166)

&lt;400&gt; 115

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tgcattttta ctctcttgac gcta atg ttc att cgg gtt tcc gct cga ccc 51
                        Met Phe Ile Arg Val Ser Ala Arg Pro
                          1                      5

gcg aca ttc gtc gag gat ttc aaa gcc gcc tgg tcg gaa tct cac atc 99
Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile
  10                      15                      20          25

cgt caa atg gaa gac gga aaa gct atc cag ctc gtc ctt gat cag agc 147
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
          30                      35                      40

act g gtacaccaac gccacagtta tatttttaaa cggaaacatt ttgaaattaa 201
Thr G

tggtgttttt atgtaatata ctctcactgt acatgttcat atttgtcttt taaag ga 258
ly

tgt gga ttt gct tcc aaa aga aaa tat cta ttc gga cga gtg agc atg 306
Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
  45                      50                      55

aag atc aaa ctc att ccc gga gac tct gcc ggt acg gtc acc gct ttc 354
Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
  60                      65                      70          75

tac gtaagtctat cattttactc cactagtgtt gaaattttac acattcacac 407
Tyr

aataaaaaat aacattttct tgaaacacta acggtcaa at cattgatatg tctatag 464

atg aac tcc gat acg gcc acg gtg aga gac gag cta gat ttt gag ttc 512
Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe
          80                      85                      90

ttg gga aac aga agt ggt caa cct tac tca gtg caa aca aac ata ttt 560
Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
          95                      100                     105

gct cat ggc aaa gga gat aga gaa caa aga gtt aat ctt tgg ttc gac 608
Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp
  110                      115                      120

cca tct atg gat tac cac act tac act atc tta tgg tca cac aaa cac 656
Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His
  125                      130                      135          140

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att gtg taagcttttc tctaattgta ctttcaacta gaatcaacat ttactgtttc 712  
Ile Val

aaaacaaaaa atcaccattt actgtttaaa aaaaccttag tttaacgtgg ggttggtttg 772

gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac 821  
Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn  
145 150 155

aac gaa gcc aag aac ata gct tac cca aca tca caa cct atg gga gta 869  
Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val  
160 165 170

tac tca aca tta tgg gaa gca gat gac tgg gca aca cgt ggt gga tta 917  
Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu  
175 180 185

gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat 965  
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp  
190 195 200

ttc gac atc gaa ggt tgt cct gtt cct gga cca acc ttt tgt cca tcg 1013  
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser  
205 210 215

aac cct cat aat tgg tgg gaa ggt tat gcc tat cag tct ctt aac gcc 1061  
Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala  
220 225 230 235

gtt gaa gct cga cgt tac cgg tgg gtt aga gta aac cat atg gtt tat 1109  
Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr  
240 245 250

gat tat tgt act gac cgg tct agg ttt cct gtc cca cca ccc gag tgt 1157  
Asp Tyr Cys Thr Asp Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys  
255 260 265

cgt gct tga aaataattgc atacgtacgt tgcaatgatc atgt 1200  
Arg Ala  
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<210> 116

<211> 269

<212> PRT

<213> Arabidopsis thaliana

<400> 116

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Lys Ala Ala Trp Ser Glu Ser His Ile Arg Gln Met Glu Asp Gly Lys  
20 25 30

Ala Ile Gln Leu Val Leu Asp Gln Ser Thr Gly Cys Gly Phe Ala Ser  
35 40 45

Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile  
 50 55 60  
 Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp  
 65 70 75 80  
 Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg  
 85 90 95  
 Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys  
 100 105 110  
 Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp Pro Ser Met Asp  
 115 120 125  
 Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr  
 130 135 140  
 Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn Asn Glu Ala Lys Asn  
 145 150 155 160  
 Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val Tyr Ser Thr Leu Trp  
 165 170 175  
 Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Glu Lys Ile Asp Trp  
 180 185 190  
 Ser Lys Ala Pro Phe Tyr Ala Tyr Lys Asp Phe Asp Ile Glu Gly  
 195 200 205  
 Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp  
 210 215 220  
 Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala Val Glu Ala Arg Arg  
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&lt;400&gt; 117

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                          1                      5

atc cgc aga acc cta acc aaa cca cac ggc act ttt tcc cgg tgt cgc 99
Ile Arg Arg Thr Leu Thr Lys Pro His Gly Thr Phe Ser Arg Cys Arg
10                      15                      20                      25

tac tta tca acc gcc gct gct gcg acg gag gtg aat tac gag gat gaa 147
Tyr Leu Ser Thr Ala Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
30                      35                      40

tcg att atg atg aaa gga gtt cga att tca ggt aga cct ctt tac tta 195
Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
45                      50                      55

gat atg caa gcg acg act ccg att gat cct aga gta ttc gat gcg atg 243
Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
60                      65                      70

aat gct tca cag atc cat gag tat ggg aat cct cac tcg cga acg cat 291
Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
75                      80                      85

ctc tac ggc tgg gaa gct gag aac gcc gtc gag aac gca cga aac cag 339
Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
90                      95                      100                      105

gtc gcg aaa ctg atc gaa gct tca ccg aag gag atc gta ttc gtg tcc 387
Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
110                      115                      120

ggt gca acg gag gcg aac aat atg gcg gtg aaa gga gtg atg cac ttt 435
Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
125                      130                      135

tac aag gac acg aag aaa cat gtg ata act aca cag act gag cat aag 483
Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
140                      145                      150

tgt gtg ctt gat tcg tgt agg cat ttg cag caa gaa gga ttt gag gta 531
Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
155                      160                      165

act tat tta cct gtg aaa act gat gga ttg gtt gat tta gag atg ttg 579
Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
170                      175                      180                      185

aga gaa gct att agg cca gac aca ggg cta gtt tct att atg gct gtg 627
Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
190                      195                      200

aac aat gag att ggt gtg gtt caa cct atg gag gag att ggt atg att 675
Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
205                      210                      215

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tgc aaa gag cat aat gtt ccg ttt cat act gat gct gct caa gct att Cys Lys Glu His Asn Val Pro Phe His Thr Asp Ala Ala Gln Ala Ile 220 225 230	723
ggg aag ata cct gtt gat gtt aag aag tgg aat gtt gct ttg atg tct Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser 235 240 245	771
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr 250 255 260 265	819
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly 270 275 280	867
ggt cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile 285 290 295	915
gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr 300 305 310	963
gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val 315 320 325	1011
aga gag aag ctt gat ggt gtt gtg gtg aat ggt tca atg gat agt cga Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg 330 335 340 345	1059
tat gta ggg aat ttg aat ttg tcg ttt gct tat gtt gaa gga gag agt Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser 350 355 360	1107
ttg ttg atg gga ttg aag gaa gtt gca gtg tct agt gga agt gct tgt Leu Leu Met Gly Leu Lys Glu Val Ala Val Ser Ser Gly Ser Ala Cys 365 370 375	1155
act agt gcg agt ttg gag cct tct tat gtg ttg aga gct ttg ggt gtg Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val 380 385 390	1203
gat gaa gac atg gct cac act tcg att agg ttt ggg att ggt agg ttt Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe 395 400 405	1251
acc acg aag gaa gag att gat aaa gcg gtc gag ctt acg gtt aaa caa Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln 410 415 420 425	1299
gtt gag aag ttg agg gaa atg agc ccg ctt tat gaa atg gtt aaa gaa Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu 430 435 440	1347
ggt atc gat atc aag aac att caa tgg tct caa cac tga ttcaacagtt	1396

Gly Ile Asp Ile Lys Asn Ile Gln Trp Ser Gln His  
445 450

cca

1399

&lt;210&gt; 118

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 118

Met Ala Ser Lys Val Ile Ser Ala Thr Ile Arg Arg Thr Leu Thr Lys  
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Pro His Gly Thr Phe Ser Arg Cys Arg Tyr Leu Ser Thr Ala Ala Ala  
20 25 30

Ala Thr Glu Val Asn Tyr Glu Asp Glu Ser Ile Met Met Lys Gly Val  
35 40 45

Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro  
50 55 60

Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu  
65 70 75 80

Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu  
85 90 95

Asn Ala Val Glu Asn Ala Arg Asn Gln Val Ala Lys Leu Ile Glu Ala  
100 105 110

Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn  
115 120 125

Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His  
130 135 140

Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg  
145 150 155 160

His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr  
165 170 175

Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp  
180 185 190

Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val  
195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro  
210 215 220

Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val  
225 230 235 240

Lys Lys Trp Asn Val Ala Leu Met Ser Met Ser Ala His Lys Ile Tyr  
 245 250 255  
 Gly Pro Lys Gly Val Gly Ala Leu Tyr Val Arg Arg Arg Pro Arg Ile  
 260 265 270  
 Arg Leu Glu Pro Leu Met Asn Gly Gly Gly Gln Glu Arg Gly Leu Arg  
 275 280 285  
 Ser Gly Thr Gly Ala Thr Gln Gln Ile Val Gly Phe Gly Ala Ala Cys  
 290 295 300  
 Glu Leu Ala Met Lys Glu Met Glu Tyr Asp Glu Lys Trp Ile Lys Gly  
 305 310 315 320  
 Leu Gln Glu Arg Leu Leu Asn Gly Val Arg Glu Lys Leu Asp Gly Val  
 325 330 335  
 Val Val Asn Gly Ser Met Asp Ser Arg Tyr Val Gly Asn Leu Asn Leu  
 340 345 350  
 Ser Phe Ala Tyr Val Glu Gly Glu Ser Leu Leu Met Gly Leu Lys Glu  
 355 360 365  
 Val Ala Val Ser Ser Gly Ser Ala Cys Thr Ser Ala Ser Leu Glu Pro  
 370 375 380  
 Ser Tyr Val Leu Arg Ala Leu Gly Val Asp Glu Asp Met Ala His Thr  
 385 390 395 400  
 Ser Ile Arg Phe Gly Ile Gly Arg Phe Thr Thr Lys Glu Glu Ile Asp  
 405 410 415  
 Lys Ala Val Glu Leu Thr Val Lys Gln Val Glu Lys Leu Arg Glu Met  
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 Gln Trp Ser Gln His  
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 <222> (8)..(1781)

<220>  
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 <222> (1833)..(2609)

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&lt;221&gt; CDS

&lt;222&gt; (2697)..(3076)

&lt;400&gt; 119

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        1             5             10

ctt ctt tct tgt ttt ctc caa gtt tct tcc aat gga gac gct gag ata 97
Leu Leu Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile
  15             20             25             30

ttg agt aga gtt aaa aag acc cga ctt ttc gac ccc gat gga aat tta 145
Leu Ser Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu
          35             40             45

caa gat tgg gtc ata acc gga gat aat cgg agt cca tgt aat tgg acg 193
Gln Asp Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr
          50             55             60

gga atc aca tgc cac atc aga aaa ggt agc tcc ctc gcc gtc act acc 241
Gly Ile Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr
          65             70             75

att gat ctc tcc ggc tat aat atc tcc ggt ggc ttt ccc tac gga ttc 289
Ile Asp Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe
          80             85             90

tgt cgt atc cgt aca ctc atc aac atc act ctt tct caa aac aat ctc 337
Cys Arg Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu
          95             100             105             110

aat ggt acg att gat tct gct cct ctc tcc ctc tgt tct aaa ctt cag 385
Asn Gly Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln
          115             120             125

aat ttg att ctc aat caa aac aac ttc tcc ggt aaa tta ccg gaa ttc 433
Asn Leu Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe
          130             135             140

tca ccg gag ttt cgt aaa tta cga gtc ctc gaa ttg gaa tca aac ctc 481
Ser Pro Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu
          145             150             155

ttc acc ggt gag att cct caa agt tac ggg aga ctc act gct ctg caa 529
Phe Thr Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln
          160             165             170

gtt ctg aat ctt aat ggt aac ccg ctc agt gga atc gtt ccg gcg ttt 577
Val Leu Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe
          175             180             185             190

ttg ggt tat ctg act gag tta act cgt ctt gat ctc gct tac atc agt 625
Leu Gly Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser
          195             200             205

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ttt gat cct agt ccg att cca tca acc ttg ggg aac ttg tcg aat ctg	673
Phe Asp Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu	
210 215 220	
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Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp	
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Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn	
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Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val	
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Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu	
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Ser Ile Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn	
290 295 300	
aat cta acc ggt gaa cta ccg gaa aag atc gct gct ctg caa ctt atc	961
Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile	
305 310 315	
tct ttc aat ctc aat gat aat ttc ttc acc gga gga tta cca gat gtc	1009
Ser Phe Asn Leu Asn Asp Asn Phe Phe Thr Gly Gly Leu Pro Asp Val	
320 325 330	
gta gct ttg aat cct aat ctc gtt gaa ttc aaa atc ttc aac aac agt	1057
Val Ala Leu Asn Pro Asn Leu Val Glu Phe Lys Ile Phe Asn Asn Ser	
335 340 345 350	
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Phe Thr Gly Thr Leu Pro Arg Asn Leu Gly Lys Phe Ser Glu Ile Ser	
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Glu Phe Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr	
370 375 380	
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Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln	
385 390 395	
tta agc ggc gaa att ccg gaa tct tac ggc gat tgt cat tcg ctt aat	1249
Leu Ser Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn	
400 405 410	
tac att cgt atg gcg gat aac aaa ctc tcc ggc gaa gtt ccg gct agg	1297
Tyr Ile Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg	
415 420 425 430	
ttt tgg gaa ctt cct ctt act cgt ctt gag cta gcc aac aac aat caa	1345

Phe Trp Glu Leu Pro Leu Thr Arg Leu Glu Leu Ala Asn Asn Asn Gln	
435 440 445	
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Leu Gln Gly Ser Ile Pro Pro Ser Ile Ser Lys Ala Arg His Leu Ser	
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Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys	
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Phe Leu Gly Ser Ile Pro Ser Cys Ile Asn Lys Leu Lys Asn Leu Glu	
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515 520 525	
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Val Ser Ser Cys Thr Glu Leu Thr Glu Leu Asn Leu Ser Asn Asn Arg	
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Tyr Leu Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu	
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Tyr G ly	
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Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg	
595 600 605	
tcc aaa cgg gaa acc ccg tac att ctg cca atc tca atc ctg tgc atc	1930
Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile	
610 615 620	
gtt gca cta acc gga gct ttg gtt tgg cta ttc atc aaa acc aaa ccg	1978
Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro	
625 630 635 640	
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Arg Val Gly Phe Thr Glu Glu Asp Ile Tyr Pro Gln Leu Thr Glu Asp	
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aac ata att ggg tcg ggc ggg tcg ggt ttg gtt tat aga gtg aaa ctc	2122
Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu	
675 680 685	
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Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly	
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Gln Lys Thr Glu Ser Glu Ser Val Phe Arg Ser Glu Val Glu Thr Leu	
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Leu Ser Tyr Leu His His Asp Ser Val Pro Pro Ile Val His Arg Asp	
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Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val	
805 810 815	
gcc gat ttc ggt tta gct aaa ccg ttg aag aga gaa gac aat gat ggt	2554
Ala Asp Phe Gly Leu Ala Lys Pro Leu Lys Arg Glu Asp Asn Asp Gly	
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gtc tcc gat gtt tca atg tct tgt gtt gct gga tcc tac ggc tac att	2602
Val Ser Asp Val Ser Met Ser Cys Val Ala Gly Ser Tyr Gly Tyr Ile	
835 840 845	
gct ccg g gttcgaattc ttagctctac aatatcaaat cgtaaacc ctatagc	2659
Ala Pro G	
850	
gcgttttagt aacattactg ttcttctgtg gatgcag aa tat ggt tat acg tca	2713
lu Tyr Gly Tyr Thr Ser	
855	



aaa gtg aat gag aag agc gat gtc tat agc ttc ggg gtg gtt tta ctc 2761  
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gaa ctg att acg gga aaa aga ccg aac gat tcg tct ttt ggg gag aat 2809  
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 Pro Ser Ala Glu Asp Gly Ala Met Asn Gln Asp Ser Leu Gly Asn Tyr  
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cga gat ctt agc aag ctt gtt gat cca aag atg aaa ctt tcg acg aga 2953  
 Arg Asp Leu Ser Lys Leu Val Asp Pro Lys Met Lys Leu Ser Thr Arg  
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Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln Leu Ser  
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 Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn Tyr Ile  
 405 410 415  
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Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly  
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 Gly Glu Glu Phe Arg Phe Leu Val Tyr Glu Phe Met Glu Asn Gly Ser  
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